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                                                                                                                                                                                                                                             Inhibition; inhibitor; protease; hepatocyte; growth factor; activation; activation; activation; activation; activation; regulation; regulation; antibody; kinetic study; assay standard; ds.
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This invention describes a preventive and/or treating agent for the diseases caused by the exasperation of activity of protease of plasma kallikrein, plasmin, urokinase and trypsin. The agent contains a protein, HAI-1 which has the following properties, M.W. of ca. 40,000 to 57,000 Dalton by SDS-PAGE and an activity of inhibiting protease activity of hepatocyte growth factor (HGF) activator. The HGF inhibiting activity on the protein is specific. HAI-1 shows a high inhibiting activity on plasmin, trypsin, HGF activator and plasma kallikrein but substantially no inhibiting activity on thrombin. This sequence encodes the human HAI-1
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treatment; prevention; protease activity; plasma; urokinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of four human protease associated proteins, designated HPRAP-1, HPRAP-2, HPRAP-3 and HPRAP-4. Human protease associated proteins are expressed in cancer and immortalised cell lines and tissues associated with inflammation and the immune response, and so appear to play a role in cell proliferative and immune disorders. The sequences can be used to diagnose, treat or prevent cell proliferative and immune disorders, including actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
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AAF30055 standard; cDNA; 2482
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                                  Human cDNA encoding PR0256
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Watanabe CK,
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standard; cDNA;
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encoding novel human immunomodulator protein PRO256 (UNQ223) {see
AAB20113). The clone was isolated from a human placenta cDNA library. The
predicted protein (58 kDa, pg 6.22) shows homology to human bixunin,
indicating protease inhibitor activity. The invention provides
polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see
AAB20108-20) including PRO256. Claimed compositions comprising their agonists are useful for increasing infiltration of for
inflammatory cells into a tissue of a mammal, stimulating or enhancing an
immune response in a mammal, or increasing the proliferation of T-
inflammatory cells into a tissue of an antigen. Claimed compositions
comprising the PRO polypeqide or its antagonist have the opposite
comprising the PRO polypeqide or its antagonist have the opposite
a T cell disorder, involves administering the PRO polypeptide, an agonist
a T cell disorder, involves administering the PRO polypeptide, an approach an antagonist antibody. The disorder is selected from
systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
clopathic inflammatory myopathy, Sjogren's syndrome, systemic
thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
chisease, demyelinated diseases (such as multiple solerosis), autoimmune
chronic active hepatitis, inflammatory biliary cirrhosis, granulomatous
chepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative
      rheumatic;
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PRO256; UNQ223; human; immune disease; autoimmune disease; antiantiarthritic; antiinflammatory; antianaemic; immunosuppressive antithyroid; antidiabetic; neuroprotective; hepatotropic; viruc dermatological; antipsoriatic; antiasthmatic; antiallergic; immunostimulant; protease inhibitor; 88.
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Pitti RM,
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colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated skin diseases (such as bullous skin disease, erythema multiforme and psoriasis), allergic diseases (such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunologic diseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease) {all claimed}. Claimed methods of diagnosing these disorders comprise detecting the level of expression of the PRO gene. Also claimed are a method of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host cells, antibodies and a method of stimulating the proliferation of T-lymphocytes
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PRO256 CDNA

activator inhibitor,

growth factor

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Human; PRO256 protein; cardiovascular; endothelial; angiogenic disorder; cardiac hypertrophy; trauma; cardiant; age-related macular degeneration; gene therapy; angiogenesis; protease activity; hepatocyte growth factor; peripheral vascular disease; hepatic; renal injury; nephrotropic; tumour restinosis; tranquillizer; vulnerary; cytostatic; hepatotropic; ss.
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2000WO-US006884.
2000US-0253665P.
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AAE09332.
                           hepatocyte
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15-MAR-2000;
28-NOV-2000;
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                                                                                 Homo sapiens
             19-NOV-2001
                                                                                                                                              mat_peptide
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P-PSDB; AA
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Wood WI

"Human hepatocyte growth factor activator PRO256"

/product= "] inhibitor, 188. .292

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/product= activator

Location/Qualifiers 188. .1777

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/*tag=

or

"Human mature hepatocyte growth fact inhibitor, PRO256"

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The present invention relates to PRO256 or its agonist/antagonist may be used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, especially a human with cardiac hypertrophy, trauma, a type of tumour or age-related macular degeneration. PRO256 may be administered together with a cardiovascular, endothelial, or angiogenic agent, a chemotherapeutic agent, a growth inhibitory agent, or a cytotoxic agent. PRO256 may also be used to treat the disorders above, preferably through administration via ex vivo gene therapy. PRO256 or its agonist may be used to inhibit endothelial cell growth, angiogenesis or protease activity of a hepatocyte growth factor, whereas an antagonist of PRO256 may be used to stimulate endothelial cell growth, angiogenesis or protease activity of a hepatocyte growth factor. Stimulation of the protease activity of a hepatocyte growth factor is proferably carried out where a mammal has a cardiovascular, endothelial, or angiogenic disorder selected from peripheral vascular disease, hepatic or renal injury or a restinosis disorder. The present sequence is human hepatocyte growth factor inhibitor, PRO256 cDNA
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sease, hepatic
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    useful for disorder.
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ted PRO256 ul
angiogenic
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    An isolated polypeptide designated cardiovascular, endothelial, or ang
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                                                                                                                                                                               Human; PRO; benign tumour; malignant tumour; lymphoid malignancy leukaemia; neuronal disorder; stromal disorder; blastocoelic disciplammatory disorder; immune disorder; angiogenic disorder; gene therapy; cytostatic; neuroprotective; gene; ss.
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2000WO-US020710.
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2000US-00664610.
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99US-0133459P.
99US-0140650P.
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99US-0145698P.
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11-MAR-1999;
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22-SEP-2000; 2000US-0235147P.
10-NOV-2000; 2000US-0235147P.
10-NOV-2000; 2000US-0235147P.
12-JAN-2001; 2001US-0261910P.
16-JAN-2001; 2001US-0261939P.
16-JAN-2001; 2001US-0264395P.
25-JAN-2001; 2001US-0264395P.
02-FEB-2001; 2001US-0264395P.
09-FEB-2001; 2001US-0264399P.
09-MAR-2001; 2001US-0282129P.
04-APR-2001; 2001US-0282199P.
04-APR-2001; 2001US-0282199P.
05-MAY-2001; 2001US-0290589P.
25-MAY-2001; 2001WO-US017092.
25-MAY-2001; 2001WO-US017800.
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genetic disorder; tum
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                                                                                                                                                                                                                                                                                                                  ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
activities, and can be used in gene therapy. The PRO polynucleotides,
cardiachypertrophs, and antagonists are useful for treating or diagnosing
a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
angiogenesis, hypertension, arterial restenssis, rheumatoid arthritis,
angiogenesis (such as breast carcinoma and liver carcinoma) and wound
healing. The PRO polynucleotides have applications in molecular biology,
including use as hybridisation probes, and in chromosome and gene
mapping. ABL88259 to ABL88267 represent primers and probes used in the
exemplification of the present invention
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J, Marstera SA,
IS PM, Wood WI,
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2001WO-USO06520.
2001US-D0802706.
2001US-D0808689.
2001US-D0816744.
2001US-D0816744.
2001US-D0828366.
2001US-D0854208.
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2001US-D0866028.
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Godowski PJ, Gurney ?
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22-MAR-2001;
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This invention relates to the cDNA and protein sequences of novel secreted and transmembrane polypeptides PRO polypeptides. The invention also comprises a method for producing the proteins of the invention by recombinant means and antibodies specific for the protein of the invention. The antibody may be used for detecting the PRO proteins of thinvention and may be used to modify their activity. polynucleotides may be used to modify their activity. polynucleotides may be used as hybridisation probes for a CDNA library to isolate the full-length PRO cDNA or to isolate other cDNAs, to construct hybridisation probes for mapping the gene which encodes that PRO and for genetic analysis of individuals with genetic disorders, in assays to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knock-out animals which in turn are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides cuseful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The sequences may also be used to detect overexpression on PRO polypeptides in cancerous tumours and for screfor differentially expressed genes using microarray technology. The present sequence represents a cDNA encoding a human PRO protein of t
                                                                                                                                                                    ) polypeptides and polymucleotides encoding the in gene therapy, chromosome identification, tiss analysis of individuals with genetic disorders
                         Filvaroff E
Stephan J,
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2000WO-US022695P.
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20-JUL-2000; 25-JUL-2000; 25-JUL-2000; 28-JUL-2000; 28-JUL-2000; 29-JUL-2000; 29-JUL-2000; 29-AUG-2000; 29-AUG-2000; 29-AUG-2000; 29-AUG-2000; 29-DEC-2000; 20-DEC-2000; 20-DE

2001US-00854280. 2001US-00866028. 2001US-00866034. 2001WO-US017092. 2001US-00870574.

1576 1636 1696 1756 160 180 200 cancer; disorder; ATCTCCAAGAAGGATGTGTTTGGCCTGAGGCGGAAATCCCCATTCCCAGCACAGGCTCT Human; angiogenesis; PRO protein; cardiovascularisation; wound, atherosclerosis; cardiac hypertrophy; gene therapy; endothelial cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiantiarteriosclerotic; gene; ss. .. 02 CDNA PRO256 206 面 2482 HisThrThrArgProLeu related entry) CDNA; (first standard; angiogenesis WO200208284-A2 Homo sapiens 19-JUL-2002 31-JAN-2002 517 161 141 1637 181 1691 201 1757 577 **ABL95581 ABL95581** Human ABL95 셤

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Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer; microvascular endothelial cell; endothelial cell tube formation; sports-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for stimulating proliferation of human microvascular endothelial cells, and PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
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The
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Zhang
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Wood WI,
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Watanabe CK,
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29-AUG-2001; 2001WO-US027099.
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Williams PM,
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30-MAY-2001; 2001WO-US017443.
01-JUN-2001; 2001WO-US017800.
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BAKER K P.
PERRARA N.
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GURNEY A L.
HILLAN K J.
MARSTERS S A.
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Watanabe
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PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The colon, breast, prostate, rectal, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polymucleotide of the invention.
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0 U; 0 Other; 709 G; 458 Ü BP; 523 A; 792 2482 Sequence

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                Conservative:
Mismatches:
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HisThrThrArgProLeu

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PRO20080 mapping,

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New isolated nucleic acid encoding a PRO polypeptide, PRO21383, useful in molecular biology, chromosome and generating antisense RNA and DNA, and in gene therapy.

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9; 308pp; English.

Claim 2; Fig

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Grimaldi JC;
Wood WI, Zhang Z;
                                                                                       human; PRO; secreted protein; transmembrane protein;
slial cell tube formation; chondrocyte cell differentiation;
sscular endothelial cell; tumour; lung tumour; colon tumour;
tumour; prostate tumour; rectal tumour; kidney tumour;
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Watanabe CK,
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P-PSDB; ADA43707.
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                                                                                                                 liver tumour;
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Gurney AL,
Fong S;
                                               ADA43706;
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tumour

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ss. PRO and
ses. The
hybridisation probe, in chromosome and gene mapping, in the genantisense RNA and DNA, and for the preparation PRO polypeptides PRO nucleic acid are useful as therapeutic agents, e.g. vaccing present sequence encodes a PRO protein.
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Other; U; 0 Ë 458 Ü 709 ΰ 792 A 523 B.P.; 2482 Seguence

1336 1396 1456 1516 1576 1636 1696 1756 121 100 120 140 160 180 200 20 40 60 80 gileHis ||||||| |CATCCAT sGluSer |||||| CGACGCC GGAGAGC BProPro gCysSer relygly |||||||| TGGTGGT SArgGly rccceec oAspAla AGGCICT GlySer MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArg 2482 200 00 04 00 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: (1-2482)ВP x ADA43706 206 2482 3.94e-114 1163.00 99.51% 99.51% 8 HisThrThrArgProLeu entry) CDNA; (1-206)(first Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: standard -390A-23 Scores 0-NOV-2003 57 1277 1337 1397 4 61 81 101 1457 121 517 577 181 147 637 201 1757 161 697 ADA43474 No. Alignment Pred. No.: US-09-935 RESULT ADA4347 셤 ద ò 8 ద d δ ò 집 ద g В Š δ ઠે ò ਨੇ ठ 8

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The invention relates to an isolated secreted/transmembrane (PRO)

polypeptide, having at least 80% sequence identity to a sequence selected
from any one of the 57 amino acid sequences given in specification, or to
a sequence encoded by a nucleic acid molecule selected from any one of
the nucleic acids deposited under any of the ATCC accession numbers given
in specification, or a sequence having at least 80% identity to PRO
can be a sequence acids of signal peptide. Also included are vectors,
transformed host cells, anti-PRO antibodise, the nucleic acids encoding
with or without its associated Signal peptide. Also included are vectors,
transformed host cells, anti-PRO antibodise, the nucleic acids encoding
with or without its associated Signal peptide. Also included are vectors,
transformed host cells, anti-PRO antibodise, the nucleic acids encoding
with or without its associated Signal peptide. Also included are vectors,
transformed host cells, anti-PRO antibodise, the nucleic acids encoding
administering PRO281, PRO2830, PRO2834 polypeptide or its agonist)
an oligonuclectide probe derived from any one of the above nucleotide
sequences. PRO6018 polypeptide is useful for stimulating the
proliferation or differentiation of fondrovyte cells, PRO313, PRO2030
and PRO2138 polypeptides are useful for stimulating the proliferation of
microvascular endothelial cells. PRO6071, PRO4487 and PRO606
colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
PRO189, PRO4499, PRO6308, PRO6000, PRO1075, PRO21207, PRO2033 and
PRO34274 polypeptides are useful for inhibiting the preparation of a
medicament for treating a condition responsive to PRO polypeptide. The
oligonuclectide sequences, for measuring or detecting the equences, or measuring or detecting the equences, or measuring or detecting the equences, and sa antisense Probes are useful for isolating genomic and sequences are useful for detecting the equences and as antisense probes. PRO polypeptides are useful as therapeutic agents, e.g. vaccines. The
proper ano
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Wood WI,
     lung tumour; ctumour; ctumour; kidney
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Watanabe CK,
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rectal t
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Stephan JP,
                    prostate tumour; recytostatic, vaccine
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Smith V,
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P-PSDB; ADA43475.
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microvascular e breast tumour; liver tumour;
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Fong S;
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Conservative: Mismatches: Indels: Gaps:

3.94e-114 1163.00 99.51% 99.51% 99.66%

Percent Similarity: Best Local Similarity Query Match:

PRO; secreted protein; transmembrane protein; tube formation; chondrocyte cell differentiati

secreted/transmembrane

cDNA encoding

ss; gene; human; endothelial cell

Alignment Scores: Pred. No.:

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tumour necrosis factor-alpha; TNP-alpha; blood; chondrocyte cell; tumo
cancer; lung; colon; breast; prostate; rectum; kidney; liver;
microvascular endothelial cell; endothelial cell tube formation.
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNN-alpha) from human blood, a method for stimulating the factor-alpha (TNN-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. lung, colon, breast, prostate, rectal, kidney and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the colypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells and for inducing endothelial cell the increase.
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with or without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, inducing endothalial cell tube formation (by administering PRO281, PRO1860, PRO4899, PRO6808, PRO68018, PRO61275, PRO21207, PRO21821 or PRO218274 polypeptide or its agonist) and can oligonucleotide probe derived from any one of the above nucleotide sequences. PRO61818 polypeptide is useful for stimulating the proliferation or differentiation of fondacocyte cells. PRO3131, PRO2183 polypeptides are useful for stimulating the proliferation of human microvascular endothalial cells. PRO6071, PRO6487 and PRO6006 and PRO2183 polypeptides are useful for inhibiting the proliferation of human microvascular endothalial cells. PRO 8019/peptides are useful for inhibiting the proliferation of human microvascular endothalial cells. PRO 8019/peptides are useful for inhibiting the prosession of luman microvascular endothalial cells. PRO 8019/peptides are useful for inducing endothalial cells tube formation. PRO or the antibody are useful in the preparation of a medicament for treating a condition responsive to PRO 8019/peptide. The oligonucleotide sequences, for measuring or detecting the expression of an associated gene, and as antisense probes. PRO 8019/peptides. PRO 9019/peptides. PRO 
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Topology: Linear;
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PN JP 1997095497-A/1
PD 08-APR-1997
PF 23-JUL-1996 JP 1996193585
PR 24-JUL-1995 JP 95P 187135
PI SHIMOMURA TAKESHI, KAWAGUCHI TOSHIYA, KITAMURA NAOMI, PI MIYAZAWA KBIJI
PC C07K14/81,C07H21/04,C07K7/06,C07K7/08,C12N5/10,C12N9/99,PC C12P21/02//A61x20/cc 212P21/02//A61x20/cc 212P21/02//cc 212P21/02//cc 212P21/02//cc 212P21/02//cc 212P21/02//cc 212P21/02//cc 212P21/02//cc 212P21/02//cc
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Mammalia, Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1542)
Shimomura, T., Kawaguchi, T., Kitamura, N. and Miyazawa, K.
NEW PROTEIN, DNA CODING THE SAME AND PRODUCTION OF THE PROP
Patent: JP 1997095497-A 1 08-APR-1997;
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C12P21/02//A61K38/55,C12Q1/68,G01N33/53,(C12P21/02,
strandedness: Double;
topology: Linear;
Teature is identified by experimental;
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Key
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/organism='Homo mapiens'
/cell line='MKN45'
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/product='HAI-I precursor'
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product='HAI-I'
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/mol_type="genomic DNA"
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JP 1997095497-A/1.
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Preventive and/or remedy for diseases caused by protease activity augmentation.
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JP 1999035480-A/1.
Homo sapiens (human)
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A61K37/24, A61K37/02, A61K37/02, A61K37/02, A61K37/02,
A61K37/547
Strandedness: Double;
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Patent: JP 1999035480-A 1 09-FEB-1999;
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Location/Qualifiers
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/db_xref="taxon:9606"
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1 (bases 1 to 1542)
Shimomura,T., Kawaguchi,T., Kitamura,N. an
Protein, DNA coding for same and method of
Patent: US 6465622-A 8 15-OCT-2002;
Location/Qualifiers
1. .1542
/organism="unknown"
/mol_type="mRNA"
                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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/organism="synthetic construct"
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This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the Sall and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after Sall site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Location/Qualifiers

Location/Qualifiers
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ELQPDRGEDAIAACFLINCLYBQNFVCKFAPREGFINYLTREVYRSYRQLKTOGFGGS
GIPKAWAGIDLKVQPQEPLVLKDVENTDWRLLRGDTDVRVERKDPNQVELWGLKEGTY
LFQLTVTSSDHPEDTANVTVTVLSTKQTEDYCLASNKVGRCRGSFPRWYYDPTEQICK
SFVYGGCLGNKNNYLREEECILACRGVQGPSMERRHPVCSGTCQPTQFRCSNGCCIDS
FLECDDTPNCPDASDEAACEKYTSGFDELQRIHFPPSDKGHCVDLPDTGLCKESIPRWY
YNPFSEHCARFTYGGCYGNKNNFEEEQQCLESCRGISKKDVFGLRREIPIPSTHWY
AVAVFLVICIVVVVAILGYCFFKNQRKDFHGHHHPPPTTPASSTVSTTEDTEHLVYNH
TTRPL"
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                                                        Hines, L., Bisenstein, S.,
Py, T., LaBaer, J., Lin, Y.,
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Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo,
1 (bases 1 to 1542)
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Bisen,
Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J.
Phelan, M. and Farmer, A.
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/codon_start=1
/product="serine protease inhibitor, Kunitz type
/protein_id="AAP36093.1"
/db_xref="G1:30583689"
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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/db_xref="taxon:9606"

/clone="GH00967X1.0"

/clone_lib="BD Creator(TM) CDS Library derived collection"

/lab_host="DH5alpha T1 resistant"
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Mismatches:
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Kalnine, N., Chen, X., Rolfs, A., Halleck,
Koundinya, M., Raphael, J., Moreira, D., F
Phelan, M. and Farmer, A.
Direct Submission
Submitted (13-MAY-2003) BD Biosciences
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                                                                                                                                              Unpublished
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Best Local Similarity:
Query Match:
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Synthetic construct
attificial sequences.

I (bases I to 1542)

Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.

Direct Submission

L chases I to 1542)

Koundinya,M., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Rolfs,M. and Farmer,A.

L chases I to 1542)

Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Roundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Roundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Roundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Direct Submission

L Submitted (02-AUG-2003) BD Biosciences Clontech, 1020 East Meadow

circle, Palo Alto, California 94303, USA

This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the Sall and HindIII sites of the
pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after
Sall site and before 'ATG' to provide Kozak consensus sequence;
'GG' after last codon and before HindIII site to maintain reading
frame. Clone distribution: http://bioinfo.clontech.com/orfclones.

Location/Qualifiers

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I. 1542
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CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC
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Losation/Qualifiers

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Location/Qualifiers

Location/Qualifiers

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                          HisThrThrArgProLeu
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Sequence 6
AR123705
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Query Match:
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Pred. No.:
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AUTHORS
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GIPKAWAGIDLKVQPQEPLVLKDVENTDWRLLRGDFDVRVERKDPNQVELWGLKEGTY
LPQLTVTSSDHPEDTANVTVTVLSTKQTEDYCLASNRVGRCRGSFPRWYYDPTEQICK
SFVYGGCLGNKNNYIRBEBCILACRGVQGPSMERRHPVCSGTCQPTQFRCSNGCCIDS
FLECDDTPNCPDASDEAACEKYTSGFDELQRIHPPSDKGHCVDLPDTGLCKESIPRWY
YNPFSEHCARFTYGGCYGNKNNPFEEEQQCLESCRGISKKDVFGLRRRIPIPSTGSVEM
AVAVFLVICIVVVVAILGYCFFKNQRKDFHGHHHPPPTPASSTVSTTEDTEHLVYNH
TTRPLL"
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                                      /lab_host="DH5alpha T1 resistant
/note="Vector: pDNR-Dual"
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Conservative:
Mismatches:
Indels:
                        CDS
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note="Mutations: 1541:Stop->L
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/db_xref="taxon:32630"
/clone="GH00967L1.0"
/clone_lib="BD Creator(TM)
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Homo sapiens (human)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2297)
Strausberg,R.L., Feingold, E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.P., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,B., Retteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Boutfard,G.G., Blakesley,R.W., Touchman,J.W., Green,B.D.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallus,D.E.,
Schmerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Processive and sequences
Processive and sequences
Processive and sequences
Processive and Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens serine protease inhibitor, Kunitz type 1, transcript variant 2, mRNA (cDNA clone MGC:1726 IMAGE:2959383), complete cds. BC004140.
BC004140.1 GI:13278722
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Strausberg, R.

Direct Submission

Submitted (01-MAR-2001) National Institutes of Health, Mammalian

Submitted (01-MAR-2001) National Institutes Office, National Cancer

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Mammalia; Eutheria; Primatee; Catarrhini; Hominidae; Homo.
1 (Dasee 1 to 1870)
Spatterson, C.
Hillman, J.L., Tang, T.Y., Lal, P., Corley, N.C., Guegler, K.J. and
Fatterson, C.
Human protease associated proteins
NAL
Human protease associated proteins
NAL
Patent: JP 2002513572-A, 2 14-MAY-2002;
INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002513572-A/2
PD 14-MAY-2002
PF 28-APR-1999 JP 2000547229
PR 01-MAY-1998 US 09/071709
PR 0
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Indels:
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Human protease associated proteins.
BD205506
BD205506.1 GI:33015276
JP 2002513572-A/2.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Butheria; Primates; Catarrh
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AB000095

Homo sapiens mRNA for hepatocyte growth factor activator inhibitor, complete cds.

AB000095

AB000095.1 GI:2924600
hepatocyte growth factor activator inhibitor.

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

B 1 (sites)

Shimomura, T., Denda, K., Kitamura, A., Kawaguchi, T., Kito, M., Kondo, J., Kagaya, S., Qin, L., Takata, H., Miyazawa, K. and Kitamura, N. Hepatocyte growth factor activator inhibitor, a novel Kunitz-type serine protease inhibitor

J. Biol. Chem. 272 (10), 6370-6376 (1997)
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Denda, K.

Direct Submission

Submitted (24-DBC-1996) Kimitoshi Denda, Tokyo Institute of
Technology, Department of Life Science; 4259 Nagatsuta, Midori-ku,
Yokohama, Kanagawa 227, Japan (E-mail:kdenda@bio.titech.ac.jp,
Tel:45-924-5702, Fax:45-924-5771)

Location/Qualifiers
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isoform 2 precursor"
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FLECDDTPNCPDASDEAACEKYTSGFDELQRIHFPPPTPASSTVSTTEDTEHLVYNH
AVAVFLVICIVVVVAILGYCFFKNQRKDFHGHHHPPPTPASSTVSTTEDTEHLVYNH
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matched mRNA gi
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This clone was selected for full length sequencing becaupassed the following selection criteria: matched mRNA girassed the following selection criteria: matched mRNA girassed the following selection criteria:
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/note="LDLa; Region: Low-density lipoprotein
domain class A"
/db_xref="CDD:smart00192"
                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Pahey, Brin Helton, Mark Kettem
Madan, Stephanie Rodrigues, Amy Sanchez and Michell
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/organism="Homo sapiens"

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/mol_type="mRNA"

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/note="Vector: pOTB7"
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/gene="SPINT1"
/note="synonyms: HAII, H7
/db_xref="LocusID:6692"
/db_xref="MIM:605123"
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/note="KU; Region: BPTI/:
inhibitors"
/db_xref="CDD:smart00131
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/note="KU; Region: BPTI
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/db_xref="CDD:cd00109"
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/codon start=1
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GIPKAWAGIDLKVQPQEPLVLKDVENTDWRLLRGDTDVRVERKDPNQVELWGLKEGTY
LFQLTVTSSDHPEDTANVTVTVLSTKQTEDYCLASNKVGRCRGSFPRWYYDPTEQICK
SFVYGGCLGNKNNYLREBECILACRGVQGPSMERRHPVCSGTCQPTQFRCSNGCCIDS
FLECDDTPNCPDASDEAACEKYTSGFDELQRIHFPPSDKGHCVDLPDTGLCKESIPRWY
YNPPSEHCARFTYGGCYGNKNNFEEEQQCLESCRGISKKDVFGLRREIPIPSTGSVEM
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/organism="Homo sapie:
/mol_type="mRNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/protein_id="AAH18702.1"
/db_xref="GI:17511686"
/db_xref="GOPPREPPEDLA REPORTABLE TO BE AGADCINS FTAGURE SPRONT SPRONT
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Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A.,
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Patent: WO 0105972-A 11 25-JAN-2001;
Genentech, Inc. (US)
Location/Qualifiers
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Stone, D.M., Watanabe, C.K. and Wood, W.I.
Compositions and methods for the treatment of
Patent: WO 0153486-A 11 26-JUL-2001;
Genentech, Inc. (US)
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Q7z7d2 homo sapien Q9d3k4 mus musculu Q99j04 mus musculu Q7xr48 oryza sativ Q8h2v9 oryza sativ Q9h813 homo sapien Q9h813 homo sapien Q9czv9 mus musculu Q9czv9 mus musculu Q9czv9 mus musculu Q9tvd1 bos taurus Q8d771 mvs musculu Q9veg2 drosophila Q9tvd1 bos taurus Q8dfq8 vibrio para Q9tl6 staphylococ O00420 homo sapien Q8xuk5 ralstonia s Descripti SUMMARIES Q7Z7D2 Q9D3K4 Q99J04 Q99J04 Q9H813 Q9H813 Q9D771 Q9D771 Q9DFQ8 Q9TVD1 Q8DFQ8 Q87RD9 Q99TL6 Q99TL6 BB \$25.50 \$2 Query Match Length ц 444 СОООООООООООООООООООООО Score Result No.

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846 16 Q8XPV0 743 5 Q9XWX5 62 5 Q26358 78 11 Q9QY97 102 5 Q9VUE1 106 16 Q8NSZ6 114 11 Q9CQH0 114 11 Q9C2H0 115 12 Q69278 125 6 Q9N123 135 16 Q97H02 136 5 Q96KR0 150 2 Q9F1P7	2 10 03975 2 10 03975 3 17 09403 3 17 09418 3 10 08427 3 16 08NNQ 5 2 09ZHW7 2 16 06958 2 17 0970N
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ALIGNMENTS

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RESULT 1 Q727D2	ID Q727D2 PRELIMINARY; PRT; 529 AA. AC 0727D2:	1-OCT-2003 (TrEMBLrel. 25, Creat	1-OCT-2003 (TrEMBLrel. 25,	01-OCT-2003 (TrEMBLrel. 25, Last	Hepatocyte growth factor aci	HAI1.	Homo sapiens (Human).	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	Mammalia; Butheria; Primates;	NCBI_TaxID=9606;		ka kadkhodayan S., Bilott J.R., Corpuz k.T., Lazarus k.A., Moran P.; Dr. grifemic commonica cantone and finite and best finite	Of HAI-1B, a	inhibitor-1.";	RN [2]	SEQUENCE FROM 1	RA Yuan J., Moran P.;	d (MAY	DR EMBL; AY296715; AAP44001.1;	Æ	cal Similarity 100.0%; Pred. No. 4.6e-150;	_	Oy 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIH				

Euteleostomi; Murinae; Mus

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STRAIN=FVB/N-3; TISSUE=Breast tumor;

KEDLINE=22388257; PubMed=12477932;

KEDLINE=22388257; PubMed=12477932;

A strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Schuler G.D.,

A popkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,

A popkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,

A popkins R.F., Jordan H., Petrner A.A., Rubin G.M., Hong L.,

A propieton M., Soares M.B., Formaldo M.F., Casavant T.L., Scheetz T.B.,

Raha S.A., McEwan P.J., Abramson R.D., Mullahy S.J.,

Raha S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

A villalon B.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz B.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

I "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=FV3/N-3; TISSUB=Breast tumor;
Strausberg R.;
Spintl.
HSSP; P05067; 1CA0.
MGD; MGI:1338033; Spintl.
GO; GO:0004867; F:Serine protease inhibitor activity; IEA.
GO; GO:0004867; F:Serine protease inhibitor activity; IEA.
InterPro; IPR002223; Kunitz BPTI.
Pfam; PF00014; Kunitz BPTI; 2.
ProDom; PD000222; Kunitz BPTI; 2.
SMART; SM00131; KU; 2.
SMART; SM00132; LDLan; 1.
                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Serine protease inhibitor, kunitz type 1 (Spintl protein)
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903{2002}.
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata
Mammalia; Eutheria; Rodentia; Sciurognathi; Murida:
NCBI_TaxID=10090;
507
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PROSITE; PS50279; BPTI KUNITZ 2;
PROSITE; PS01209; LDLRA 1; 1.
PROSITE; PS50068; LDLRA 2; 1.
PROSITE; PS50068; LDLRA 2; 1.
PROTERE 507 AA; 56590 MW: P77
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larity 100.0%; F.
Conservative 0;
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SIGNENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Head;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Kadoka J., Fukuda S.,

A Arakawa T., Hara A., Ashburner M., Batalov S., Yamanaka I.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

R Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

R Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Austonich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Harsedin S., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Harsehisabiashi V.
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NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;

Hayashizaki Y.;

"Functional annotation of a full-length mouse cDNA collection.";

Nature 409:685-690(2001).

EMBL; AK017342; BAB30697.1; -.

HSSP; P05067; 1CA0.

MGD; MGI:1338033; Spint1.

GO: GO:0004867; F:serine protease inhibitor activity; IBA.

InterPro; IPR002223; Kunitz_BPTI.

InterPro; IPR002172; LDL receptor_A.

Pfam; PF00014; Kunitz_BPTI; 2.

Pfam; PF00057; Idl recept a; 1.

PRINTS; PR00759; BASICPTASE.

Probom; PD000222; Kunitz_BPTI; 2.

SMART; SM00131; KU; 2.
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PS50279; BPTI KUNITZ 2; 2.
PS01209; LDLRA 1; 1.
PS50068; LDLRA 2; 1.
inhibitor; Serine protease inhibitor.
507 AA; 56571 MW; 9EE0A29B7056D72D CRC64;
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Last sequence update)
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Pred. No.
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                                19.4%; SC.
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01-JUN-2001
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[1] SEQUENCE

Q9D3K4

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inhibitor; Serine protease inhibitor. 56590 MW; F7F9CCF2693D1F8D CRC64;
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Shang N., Kang H., Chen X.Y.,

Shang Y., Cai Z., Chen J., Kang H., Chen X.Y.,

Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhang W., Wang L.J., Ding C.W.,

A Chen L., Pan D.L., Weng Q.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,

Chen L., Pan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,

Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,

A Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,

A Zhang R.Q., Guan J.P., Hong G.F.;

Shang R.Q., Guan J.P., Hong G.F.;
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OSJNBB0011B04.11 protein.
OSJNBB0011B04.11.
OSJNBB0011B04.11.
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
                      O7XR48

O7XR48;

O7XR48;

O7XR48;

O1-OCT-2003 (TrEMBLrel. 25, Created)

O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)

O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)

O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)

OSJNBA0043A12.37

OSJNBA0043A12.37.

Oryza sativa (Rice).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Shrhartoideae; Oryzeae; Oryza.
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STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chrclone:OSJNBb0011E04.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ EMBL; AP005443; BAC22566.1; -.
SEQUENCE 250 AA; 27639 MW; 60DA333BAD5822F
                                                                                                                                                                                                                                                                                                                                                                                                  Score 9; DB 10;
Pred. No. 0.55;
0; Mismatches
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                                                                                                                                                                                         SEQUENCE FROM N.A.

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Kanehori K.; "NEDO human cDNA sequencing project."; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AK001736; BAA91870.1; -.

Hypothetical protein.

SEQUENCE 350 AA; 39956 MW; D7B5875C34C9398C CRC64;
                                                                                                         Buteleostomi;
Homo.
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                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
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O9H813
O9H813
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O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ14004.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; BMammalia; Butheria; Primates; Catarrhini; Hominidae;
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Last sequence update)
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Straubberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
EMBL; AK024066; BAB14810.1; -.
EMBL; BC006320; AAH06320.1; -.
Hypothetical protein.
SEQUENCE 350 AA; 40043 MW; 5F68ACA21DDD067
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red. No. 6.3;
Mismatches
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Pred. No. 6.3;
0; Mismatches
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01-OCT-2000 (TrEMBLrel. 15, La
01-OCT-2002 (TrEMBLrel. 22, La
Hypothetical protein FLJ10874.
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8; Conserv
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SEQUENCE PROM N.A
TISSUE=Muscle;
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STRAIN=C57BL/6J; TISSUE=Embryo;

MEDLINE=21085660; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Isawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

Kacota K., Matsud H.A., Ashburner M., Batalov S., Casavant T.,

Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,

Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio A Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,

B Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P.,

A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,
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L., Washio
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MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of a full-length mouse cDNA collection.
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EMBL, AX012107, BAB28038.1; -.

MGD, MGI:1914200, 2310028N02Rik.

SEQUENCE 350 AA; 40285 MW; 12FD43319660775B CRC64;
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Sciurognathi; Muridae;
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i; Muridae;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
2310028N02Rik protein (RIKEN CDNA 2310028N02 gene)
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Pred. No. 6.3;
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Sciurognathi
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Mammalia; Eutheria; Rodentia;
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Mammalia, Eutheria, Rodentia,
NCBI_TaxID=10090;
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Q9CZV9;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
2310028N02Rik protein.
2310028N02Rik.
Mus musculus (Mouse).
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2310028N02RIK.
Mus musculus (1
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SEQUENCE
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Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.,
Functional annotation of a full-length mouse cDNA collection.";
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Champe M., Pfeiffer B.D.
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G
Wan K.H., Doyle C., Baxter R.G., An H.-J., Andrews-Pfannkoch C., Baldwin D.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/63; TISSUE=Retina, Spinal cord, and Testis;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Tea
"Analysis of the mouse transcriptome based on functional ann
60,770 full-length cDNA9.";
Nature 420:563-573(2002).
EMBL; AK009526; BAB26340.1; -.
EMBL; AK031270; BAC27330.1; -.
EMBL; AK044482; BAC31946.1; -.
EMBL; AK0446482; BAC31946.1; -.
EMBL; AK045641; BAC33853.1; -.
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Pred. No. 6.
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(TrEMBLrel. 24, I
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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M., Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkockan D., Borkstein P., Brottier P., Burtis K.C. Busam D.B., Bouler H., Cadieu E., Center A., Chandra I., Charler J. Burtis K.C. Busam D.B. Dalke C., Davenport L.B., Davies P., Chandra I., Charler J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Davies B., Dalcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodon K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Perrisa S., Platschmann W., Roller C., Gabrielian A.B., Garg N.S., Galbart W.M., Glasser K., A. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Harvey D., Heiman T.J., Hernandez J.R., Hock J., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalai M., Malush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McDerson D.L., Mourt S.M., Mattei B., McIntosh T.C., McLeod M.P., McDerson D.L., Molson K., Nusskern D.R., Pacle D. M., Nelson D.L., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shie B., Strand A., Supski M.P., Sauth T., Shie B., Syriskas R., Tector C., Turner R., Venter E., Mang A.H., Wang X., Mang Z.-Y., Wassarran D.A., Weinstock G.M., Weissenbach J., Sylber B., Strand S., Zaveri J.S., Zhan M., Zhang S., Zao Q.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Woodage T., Wooley C., Stang G., Zhao Q., Zhang G., Zhao G., Shenge C., Shenge C., Shenge C., Shenge C., Shenge C., Shenge C., Stang G., Zhao Q., Zhang G., Zhao G., Shenge C., S
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Gelniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Gelniker S.E., Adams M.D., Ananatides P.G., Brandon R.C., Rogers Y.,

Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Numoo J.,

Rapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,

"Sequencing of Drosophila melanogaster genome.",

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A., Matthews B.B., Bayraktaroglu L., Campbell Hradecky P., Grosby M.A., Kaminker J.S., Prochnik S.E., Smith C.D. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.

Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris I Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E "Annotation of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ Gatabases.
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB003719; AAF55462.2; -.
FlyBase; FBgn0038541; CG16766.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
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Submitted (MAR-2000)
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dopamine beta
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Wu H.J., Parmer R.J., Koop A.H., Rozansky D.J., O'Connor D. Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF118638; AAD09829.1; -.

HSSP; P14925; IPHM.

GO; GO:0005507; F:copper ion binding; IEA.

InterPro; IPR000323; Cu2 monooxygenase.

InterPro; IPR000945; DB monoxygenase.

InterPro; IPR008977; PHM PNGase F.

InterPro; IPR008977; PHM PNGase F.

Pfam; PF01082; Cu2 monooxygen; 1.

Pfam; PF0351; DOMON; 1.
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DOPAMINE BETA-HYDROXYLASE.
CF89D62A9472B7C6 CRC64;
Pfam; PF00001; 7cm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
SEQUENCE 586 AA; 64897 NW; BEB9C75EE6B3844F CRC64;
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on update)
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TISSUB=Adrenal medulla;

MEDLINE=90285664; PubMed=1693949;

Wu H.J., Parmer R.J., Koop A.H., Rozansky D.J., C
"Molecular cloning, structure, and expression of hydroxylase from bovine adrenal medulla.";
J. Neurochem. 55:97-105(1990).
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Pred. No. 9.9;
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Mismatches
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Pred.
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SMART; SM00664; DOH; 1.
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100.0%;
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8; Conservative
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8; Conservative
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597 AA;
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5 AVAVFLVI
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PROSITE; PS00084;
PROSITE; PS00085;
                                                                                                                     144 AVAVELVI
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01-MAY-2000
01-OCT-2003
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Best Local
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Length

16;

DB 16

Score 8; DB 1 Pred. No. 12; 0; Mismatches

CRC64;

BEB6E07BCEB8663D

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3.9%; Sc.
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8; Conservative
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     Complete proteome. SEQUENCE 758 AA;
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516 IVVVVAIL
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STRAIN=RIMD 2210633 / Serotype O3:K6;

MEDLINE=22508454; PubMed=12620739;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagom Ijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kim Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic med distinct from that of V. cholerae.";

"Genome sequence of Vibrio parahaemolyticus: a pathogenic med distinct from that of V. cholerae.";

EMBL; AP005075; BAC59121.1; -.

GO: GO:0015093; F: Ferrous iron transporter activity; IEA.

GO: GO:0015684; P: Ferrous iron transport; IEA.

R InterPro; IPR006073; GTP1_OBG.
                                                                                                                                                                                                                                      Jeong
                                                                                                                Vibrio vulnificus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=672;
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=670;
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
transport protein B.
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rt system protein B.
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Pred. No. 12;
0; Mismatches
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; TIGR00231; small_GTP;
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8; Conserv
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01-MAR-2003 (Tr)
01-JUN-2003 (Tr)
Fe2+ transport :
VV10148.
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01-JUN-2003 (7
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SEQUENCE FROM
STRAIN=CMCP6;
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TIGRFAMS;
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Pfam; PF02
PRINTS; PR
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Best Local S
Matches
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WEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi J. Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi J., Cguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C. Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shi Hattori M., Ogasawara N., Hayashi H., Hiramatsu K., Yoshino C., Shi "Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
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Q99TL6 PRELIMINARY; PRT; 759 AA.
Q99TL6;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Protein-export membrane protein SecDF.
SECF OR SAV1637 OR SA1463 OR MW1587.
Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain N315), and
Staphylococcus aureus (strain NW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879, 196620;
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Similarity 100.0%;
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Lamerdin J.B., McGready P.M., Adamson A.A., Burkhart-Schultz K.,
Lamerdin J.B., McGready P.M., Stilwagen S., Garnes J., Danganan I.

Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan I.

Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
A. Carrano A.V.;
"Sequence analysis of a 1 MD region in human 19q13.1.";
"Sequence analysis of a 1 MD region in human 19q13.1.";
"Sequence analysis of a 1 MD region in human 19q13.1.";
"Sequence analysis of a 1 MD region in human 19q13.1.";
"Sequence analysis of a 1 MD region in human 19q13.1.";
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"Sequence analysis of a 1 MD region in human 19q13.1.";
"Sequence analysis of a 1 MD region in human 19q13.1.";
"Go; Go: 0004557; Proline dehydrogenase activity; IEA.
GO; GO: 00065509; Proline catabolism; IEA.
GO; GO: 00065509; Proline catabolism; IEA.
RoinerPro; IPR002872; Pro_dh.
RoinerPro; IPR002872; Pro_dh.
RoinerPro; IPR002872; Pro_dh.
RoinerPro; IPR00138; SUBTILASE_SER; 1.
RoinerPro; IPR00772; Pro_dh.
RoinerPro; IPR0772; Pro_dh.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
F19541_1 (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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US-09-935-390A-23 206 1 MERRHPVCSGTCQPTQFRCS.....TVSTTEDTEHLVYNHTTRPL Title: Perfect score: Seguence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

141681 seqs, 52070155 residues Searched:

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141681 Total number of hits satisfying chosen parameters:

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SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pand is derived by analysis of the total score distribution.

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                   This SWISS-PROT entry is copyright. It is produced through a collaborabetween the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/announce send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Secreted.

DOMAIN: This inhibitor contains two inhibitory domain SIMILARITY: Contains 1 LDL-receptor class A domain. SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains
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EMBL; BC004140; AAH04140.1; -.
EMBL; BC018702; AAH18702.1; -.
HSSP; P31713; 1SHP.
Genew; HGNC:11246; SPINT1.
MIM; 605123; -.
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Matches 206; Conservative
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**Andres G., McCluskey R.T.;

**Cogan distribution in rate of two members of the low-density lipoprotein receptor gene family, gp330 and LRP/alpa 2MR, and the receptor-associated protein (RAP).";

**Complex Binds plasminogen, extracellular matrix components, plasminogen activator-plasminogen activator inhibitor type I complex, apolipoprotein B-enriched beta-VDDL, lipoprotein lipas lactoferrin, clusterin and calcium.

**Complex Binds plasminogen, extracellular matrix components, plasminogen activator-plasminogen activator inhibitor type I complex, apolipoprotein B-enriched beta-VDDL, lipoprotein lipas lactoferrin, aminoglycosides and polymyxin B.

-!- FUNCTION: Receptor-mediated uptake of polybasic drugs such as aprotinin, aminoglycosides and polymyxin B.

-!- SUBUNIT: Forms a multimeric complex together with a receptor-associated protein (RAP). Binds to ankyrin-repeat family A protein clasvage at the cell surface.

-!- SUBCELLULAR LOCATION: Type I membrane protein. Expressed in clarkrin-coated pits; a soluble form is possibly derived by cleavage at the cell surface.

-!- TISSUE SPECIFICITY: Epithelial cells of kidney glomerulus and proximal tubule, lung, epididymis, yolk sac, among others.

-!- SIMILARITY: Contains 37 LDL-receptor class A domains.

-!- SIMILARITY: Contains 17 EGF like domains.
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Moestrup S.K., Cui S., Vorum H., Bregengaard C., Bjorn S.B.,
Norris K., Gliemann J., Christensen B.I.;
"Evidence that epithelial glycoprotein 330/megalin mediates upto
polybasic drugs.";
J. Clin. Invest. 96:1404-1413(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Buteleostom
Sciurognathi; Muridae; Murinae; R
                                                                                                                                                                                                                                       precursor
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SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley, TISSUE=Kidney,
MEDLINE=95024033; PubMed=7937880;
Saito A., Pietromonaco S., Loo A.K.C., Farquhar M.G.,
Saito A., Pietromonaco S., Loo A.K.C., Farquhar M.G.,
"Complete cloning and sequencing of rat gp330/'megalin,' a
"Complete cloning and sequencing of rat gp330/'megalin,' a
                                         433
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CARFTYGGCYGNKONNPBEBQQCLESCRGISKKDVPGLRRE
                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Low-density lipoprotein receptor-related protein
(Glycoprotein 330) (gp330).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91:9725-9729(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94172242; PubMed=7510321;
Zheng G., Bachinsky D.R., Stamenkovic I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
96:1404-1413(1995)
                                                                                                                                                                                                                                                                 iRP2.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Ci
Mammalia; Butheria; Rodentia; Son NCBI_TaxID=10116;
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TISSUE SPECIFICITY
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ID _LRP2_RAT
AC P98158;
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(Dopamine beta-

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SEQUENCE FROM N.A.
MEDLINE=90148928; PubMed=2620060;
Taljanidisz J., Stewart L., Smith A.J., Klinman J.P.;
Taljanidisz J., Stewart L., Smith A.J., Klinman J.P.;
Taljanidisz J., Stewart L., Smith A.J., Klinman J.P.;

"Structure of bovine adrenal dopamine beta-monooxygenase, as deduced from cDNA and protein sequencing: evidence that the membrane-bound from of the enzyme is anchored by an uncleaved signal peptide.";
Biochemistry 28:10054-10061(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE OF 33-610.
MEDLINE=90110082; PubMed=2295597;
Robertson J.G., Desai P.R., Kumar A., Farrington G.K.,
Fitzpatrick P.F., Villafranca J.J.;
"Primary amino acid sequence of bovine dopamine beta-hydroxylase.";
"Primary amino acid sequence of bovine dopamine beta-hydroxylase.";
J. Biol. Chem. 265:1029-1035(1990).
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
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TISSUE=Adrenal medulla;
MEDLINE=77134133; PubMed=843373;
Skotland T., Ljones T., Flatmark T., Sletten K.;
"NH2-terminal sequence of dopamine beta-hydroxylase from bovine adrenal medulla.";
Biochem. Biophys. Res. Commun. 74:1483-1489(1977).
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MEDLINE=89079641; PubMed=2909511;
Taylor C.S., Kent U.M., Fleming P.J.;
"The membrane-binding segment of dopamine beta-hydroxylase uncleaved signal sequence.";
J. Biol. Chem. 264:14-16(1989).
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MEDLINE=90110081; PubMed=1688549;
Lewis E.J., Allison S., Fader D., Claflin V., Baizer L.;
"Bovine dopamine beta-hydroxylase cDNA. Complete coding stexpression in mammalian cells with vaccinia virus vector."
J. Biol. Chem. 265:1021-1028(1990).
   DOPO BOVIN STANDARD; PRT; 610 AA.
P15101;
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Dopamine beta-monooxygenase precursor (BC 1.14.17.1)
hydroxylase) (DBH),
                                                                                                                                                                   (Bovine).
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MEDLINE=95001861; PubMed=7918370;
Robertson J.G., Adams G.W., Medzihradszky K.F., Burlingar Villafranca J.J.;
Complete assignment of disulfide bonds in bovine dopamin hydroxylase.";
Biochemistry 33:11563-11575(1994).
-!- FUNCTION: Conversion of dopamine to noradrenaline.
-!- CATALYTIC ACTIVITY: 3,4-dihydroxyphenethylamine + asc.
-!- CATALYTIC ACTIVITY: 3,4-dihydroxyphenethylamine + asc.
-!- COPACTOR: PQQ, copper and ascorbate + H(2)0.
-!- COPACTOR: PQQ, copper and ascorbate.
-!- SUBUNIT: Homotetramer.
-!- SUBUNIT: Homotetramer.
-!- SUBCELLULAR LOCATION: Exists both in a soluble form granules) and as membrane bound (the membrane bound anchored by an uncleaved signal peptide).
-!- SIMILARITY: Belongs to the copper type II, ascorbatemonoxygenase family.
-!- SIMILARITY: Contains 1 DOMON domain.
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060500;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Nephrin precursor (Renal glomerulus-specific cell adhesion recepton NPHS1 OR NPHN.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
between the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute. There are no restrictives by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.clor send an email to license@isb-sib.ch).
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Aya K., Tanaka H., Seino Y.;

Aya K., Tanaka H., Seino Y.;

"Novel mutation in the nephrin gene of a Japanese patient with congenital nephrotic syndrome of the Finnish type.";

Kidney Int. 57:401-404(2000).

-!- FUNCTION: Seems to play a role in the development or function of the kidney glomerular filtration barrier. May anchor the podocyte slit diaphragm to the actin cytoskeleton.

-!- SUBUNIT: Interacts with podocin/NPHS2. Interacts with CD2AP C-terminal domain (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

Predominantly located at podocyte slit diaphragm between podocyte foot processes. Also associated with podocyte apical plasma membrane.
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MEDLINE=99115081; PubMed=9915943; Lenkkeri U., Maennikkoe M., McCready P., Lamerdin J., Gribouval C Niaudet P.M., Antignac C.K., Kashtan C.E., Homberg C., Olsen A., Kestilae M., Tryggvason K.; "Structure of the gene for congenital nephrotic syndrome of the Finnish type (NPHSI) and characterization of mutations."; Am. J. Hum. Genet. 64:51-61(1999).
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98325371; PubMed=9660941;
Kestilae M., Lenkkeri U., Maennikkoe M., Lamerdin J., McCready
Putaala H., Ruotsalainen V., Morita T., Nissinen M., Herva R.,
Kashtan C.E., Peltonen L., Holmberg C., Olsen A., Tryggvason K.
"Positionally cloned gene for a novel glomerular protein -- negis mutated in congenital nephrotic syndrome.";
Mol. Cell 1:575-582(1998).
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Grunkemeyer J.A., Kumar N., Kalluri R.;
"Human nephrin (NPHSI) cDNA sequence.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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Event=Alternative splicing; Named isoforms=2;
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Ruotsalainen V., Ljungberg P., Wartiovaara J., Le
Kestilae M., Jalanko H., Holmberg C., Tryggvason
"Nephrin is specifically located at the slit diap
podocytes.";
Proc. Natl. Acad. Sci. U.S.A. 96:7962-7967(1999).
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TISSUE SPECIFICITY: Specifically expressed
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MEDLINE=21551283; PubMed=11562357;
Huber T.B., Kottgen M., Schilling B.,
"Interaction with podocin facilitates
J. Biol. Chem. 276:41543-41546(2001).
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SEQUENCE OF 1032-1134 FROM N.A. (IS
MEDLINE=20019662; PubMed=10550324;
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MEDLINE-20117947; PubMed=10652016;
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Archaeo; Buryarchaeota; Archaeoglobi; Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
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SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Klenk H.-P., Clayton R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AP0585.
AP0585.
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ch/announce,
                                         congenital nephrotic [MIM:256300]; an by massive proteinuria
                                                                                                                                                                                                                            iona on
podocytes of the periphery of mature and developing glomeruli.

-!- PTM: Phosphorylated on tyrosine residues.
-!- DISEASE: Defects in NPHS1 are the cause of congenital nephrotic syndrome of the Finnish type (NPHS1 or CNF) [MIM:256300]; an autosomal recessive disorder characterized by massive proteinur in utero and nephrosis at birth.
-!- SIMILARITY: Belongs to the immunoglobulin superfamily.
-!- SIMILARITY: Contains 1 fibronectin type III domain.
-!- SIMILARITY: Contains 8 immunoglobulin-like domains.
-!- SIMILARITY: Contains 9 immunoglobulin-like domains.
-!- SIMILARITY: Contains 8 immunoglobulin-like domains.
-!- SIMILARITY: Contains 9 immunoglobulin-like domains.
-!- SIMILARITY: Selong 9 immunoglobulin-like domains.
-!- SIMILARITY: Selong 9 immu
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          glomeruli
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BXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 7.

IG-LIKE C2-TYPE 7.

IG-LIKE C2-TYPE 9.

IG-LIKE C2-TYPE 9.

IG-LIKE C2-TYPE 9.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 9.

IG-LIKE C2-TYPE 9.

IG-LIKE C2-TYPE 9.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 9.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 1.
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       B.,
Zhou 1.,
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E
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Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus E Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zh Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome
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POTENTIAL.
CSD18CF7C03B4226 CRC64;
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Pred. No. 3.5;
; Mismatches
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TIGR; AF0585; -.

Hypothetical protein; Transmembrane; Cc
TRANSMEM 5 27 POTENTIAL.

TRANSMEM 40 62 POTENTIAL.

TRANSMEM 67 89 POTENTIAL.
                                                                                                                                                                                "The complete genome sequence of threducing archaeon Archaeoglobus ful Nature 390:364-370(1997).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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89
10081 MW;
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7; Conserv
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                                                                                                                                                                                                                                                                         CHARACTERIZATION.

MEDLINE=96312852; PubMed=8701988;

A Kocher O., Cheresh P., Lee S.W.;

"Identification and partial characterization of a novel membrane-
"I associated protein (MAPI7) up-regulated in human carcinomas and
"I modulating cell replication and tumor growth.";

L Am. J. Pathol. 149:493-500(1996).

-1- FUNCTION: May play an important role in tumor biology.

-1- FUNCTION: May play an important role in tumor biology.

-1- TISSUE SPECIFICITY: Expressed at significant levels only in a single epithelial cell population, the proximal tubular epithelial cells of the kidney. Diffusely expressed in various carcinomas originating from kidney, colon, lung and breast.
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Batterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales
Enterobacteriaceae; Escherichia.
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-> K (IN REF. 3).
7DEB64C3AF78CB18 CRC64;
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P77551;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Putative Rz endopeptidase from lambdoid prophage Rac (Fragment).
RZPR OR B1362.
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Pred. No. 4.4
0; Mismatches
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T -> M (IN
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12227 MW;
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Best Local Similarity 100.0%;
Matches 7; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; UZ1049; AAA92690.1; -.
EMBL; AL135960; CAB72104.1;
EMBL; BC012303; AAH12303.1;
MIM; 607178; -.
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13
51
114 AA;
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ID RZPR E
AC P77551
DT 16-OCT
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(Potential)

protein

LOCATION: Integral membrane Belongs to the dedA family.

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390a-23

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SUBCELLULAR SIMILARITY:
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Proc. Natl.
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Best Local
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                                                                                                                                                                                                                                                                                                                                          EMBL;
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Matches
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Saito N.,
                                                                                                                                                                                                                                                                                                                                              Itoh T.,
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus
NCBI_TaxID=1359;
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3-link
the
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                                                                                                                                                                                                                                                                 STRAIN=K12;

Kabine 1. Submed=9097039;

Kabine 1. Fujita K., Hayashi K., Inada T., Isono K., Itoh Kasai H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh Kasai H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh Kasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M., Kasai H., Rashimoto K., Makamura Y., Nashimoto H., Nishio Y., Oshima T., Saito Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; A Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map."; DNA Res. 3:363-377(1996).

C. -!- FUNCTION: Necessary for host cell lysis. It is believed to conform endopeptidase that cleaves the amino-carboxyl cross-line for an endopeptidase that cleaves the amino-carboxyl cross-line murein component of the bacterial cell wall (By similarity).

C. -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY UB. STRONG, TO LAMBDO PHAGES ENDOPEPTIDASES.
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                                   면 E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL on the Buropean Bioinformatics Institute. There are no restrictivuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.clor send an email to license@isb-sib.ch).
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burlan
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=MG1363;
Venema K., Haandrikman A., Leenhouts K., Kok J., Venema G.;
Venema K., Haandrikman A., Leenhouts K., Kok J., Venema G.;
Venema K., Haandrikman A., Leenhouts K., Kok J., Venema G.;
"Cloning and sequencing of a gene (apl) from Lactococcus lacticoning and sequencing of a gene (apl) from Lactococcus lactical complement a phoA mutation in Escherichia coli.";
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                       "The complete genome sequence of Bacherichia coli K-12."; Science 277:1453-1474(1997).
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on update)
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Pred. No. 5.5;
0; Mismatches
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InterPro; IPR004929; Phage lysis.
Pfam; PF03245; Phage_lysis; 1.
Hypothetical protein; Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
28-FBB-2003 (Rel. 41, Last annotation
Alkaline phosphatase like protein.
APL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; AAC74444.1; ALT INIT.
BAA14959.1; ALT_INIT.
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7; Conservative
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EMBL; D90774; B
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Q48630;
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Best Local
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
through a collaboracing the EMBL outstation
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TISSUE=Bye, and Kidney;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi; Homo.
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V W.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISSUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
FISSUE=Renal cell carcinoma;
MEDLINE=98301622; PubMed=9636197;
Tuereci O., Sahin U., Vollmar E., Siemer S., Goettert E., Sei Parkkila A.-K., Shah G.N., Grubb J.H., Pfreundschuh M., Sly Fluman carbonic anhydrase XII: cDNA cloning, expression, and chromosomal localization of a carbonic anhydrase gene that is overexpressed in some renal cell cancers.";
Proc. Natl. Acad. Sci. U.S.A. 95:7608-7613(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Carbonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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POTENTIAL.
POTENTIAL.
650A8B314C44BA55 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAHC HUMAN STANDARD; PRT; 354 AA. 043570; Q9BWG2; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Carbonic anhydrase XII precursor (EC 4.2.1.1) XII) (CA-XII) (Tumor antigen HOM-RCC-3.1.3). CA12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ore 7; DB 1;
red. No. 8.7;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7;
Pred. No.
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TISSUE=Lung;
MEDLINE=98445416; PubMed=9770531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                      68 P
161 P
197 P
27134 MW;
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                                                                                                                                                                                                                       Z29065; CAA82306.1;
                                                                                                                                                                                                                                           PIR; S39339; S39339.
InterPro; IPR000252; Deda
Pfam; PF00597; Deda; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 100
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186
                                                                                                                                                                                                                                                                                                                                                                                                                                 242 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collaboration
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
Vihlalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rhiting M., Madan J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J.M., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J.M., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J.M., Myers R.M.,
Rodriguez A.C., Grimwood J.M., Rodriguez R.M.,
Rodr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=2;
Isold=043570-2; Sequence=VSP_000772;
Note=No experimental confirmation available;
Note=No experimental confirmation available;
INTESTINE AND ACTIVATED LYMPHOCYTES. EXPRESSED AT MUCH HIGHER
LEVELS IN THE RENAL CELL CANCERS THAN IN SURROUNDING NORMAL KIDNEY
TISSUE. MODERATELY EXPRESSED IN PANCREAS, OVARY, AND TESTIS.
SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 30-292.

MEDLINE=21396545; PubMed=11493685;
Whittington D.A., Waheed A., Ulmasov B., Shah G.N., Grubb J.H.,
Sly W.S., Christianson D.W.;
"Crystal structure of the dimeric extracellular domain of human
carbonic anhydrase XII, a bitopic membrane protein overexpressed in
certain cancer tumor cells.";
Proc. Natl. Acad. Sci. U.S.A. 98:9545-9550(2001).
-!- FUNCTION: Reversible hydration of carbon dioxide.
-!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
-!- COPACTOR: Zinc (By similarity).
-!- ENZYME REGULATION: Inhibited by acetazolamide.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 것
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REMBL; AF051882; AAC39789.1; -..

REMBL; BC000278; AAC3952.1; -..

REMBL; BC000278; AAH1691.1; -..

REMBL; BC002381; AAH1691.1; -..

REMBL; BC023981; AAH1691.1; -..

REMBL; BC023981; AAH1691.1; -..

REMBL; BC00238; AAH1691.1; -..

REMBL; BC001601; Callegral to membrane; TAS.

GO; GO:0004089; F:carbonate dehydratase activity; TAS.

GO; GO:0004089; F:carbonate dehydratase activity; TAS.

GO; GO:0004089; F:carbonate dehydratase activity; TAS.

GO; GO:0008270; F:zinc ion binding; TAS.

InterPro; IPR001148; Buk Coanhd.

ProDom; PD000865; EUK CO2 ANHYDRASE; 1.

PROSITE; PS00162; EUK CO2 ANHYDRASE; 1.

Lyase; Zinc; Transmembrane; Signal; Alternative splicing; SIGNAT.
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
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IsoId=043570-1; Sequence=Displayed;
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                  N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
Missing (in isoform 2
/FTId=VSP_000772.
(CATALYTIC). (CATALYTIC). (CATALYTIC).
                                                                                                                                                                                                                                                                                                             RESULT 11
QIN AVIS3
ID QIN AVIS3
STANDARD; PRT; 387 AA.
AC P56260;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT ZB-FEB-2003 (Rel. 41, Last annotation update)
DT Transforming protein Qin (Oncogene Qin).
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Pred. No. 12;
0; Mismatches
ZINC
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Best Local Similarity 100
Matches 7; Conservative
1119
1121
145
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316 ICIWWW 322
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Gallus.
NCBI_TaxID=9031;
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763
1122
1182
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В.
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STRAIN=Rd / KW20 / ATCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick Ferlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick Ferlavage A.R., Bult C.J., Fitzhugh W., Fields C.A., Gocayne J.D.
                                                                                                                                   fact
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                                  retroviru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BRNO OR HI0226.
Haemophilus influenzae.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                  A GAG-QIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carrier protein
                                                                           MEDLINE=93281605; PubMed=8099441;
Li J., Vogt P.K.;
The retroviral oncogene gin belongs to the transcription family that includes the homeotic gene fork head.";
Proc. Natl. Acad. Sci. U.S.A. 90:4490-4494(1993).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-QI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORK-HEAD.
FEA902F50FFE42F9 CRC64;
                                 Ç
              Avian sarcoma virus (strain 31) (ASV31).
Viruses, Retroid viruses, Retroviridae, Avian type
NCBI_TaxID=35270;
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system can
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red. No. 13;
Mismatches
                                                                                                                                                                                                                POLYPROTEIN. SIMILARITY: Contains 1 fork-head domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Branched-chain amino acid transport system
chain amino acid uptake carrier).
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larity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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P71345;
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                                                                                                                                                                                                                                    đ
                                                                                                                                       influenzae
                                                                                                                                                          Rd.";
Science 269:496-512(1995).
-!- FUNCTION: Component of the transport system for branched-chain amino acids (leucine, isoleucine and valine) Which is coupled to proton motive force (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: BELONGS TO THE BRAC/BRAZ/BRNQ FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata, Vertebrata, Euteleostomi,
Galliformes, Phasianidae, Phasianinae
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D. Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U32709; AAC21896.1; -.
PIR; D64056; D64056.
TIGR; H10226; -.
InterPro; IPR004685; Livcs.
Pfam; PF05525; Branch AA trans; 1.
TIGRFAMS; TIGR00796; Tivcs; 1.
Amino-acid transport; Transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                       of Haemophilus
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(CBF-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 436;
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090964;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Forkhead box protein GlB (Forkhead-related protein FKB (Transcription factor BF-1) (Brain factor 1) (BF1) (CB oncogene C-QIN) (N-62-5) (CEQ 3-1).
FOXGIB OR FKH11 OR QIN.
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Evactosauria; Aves; Neognathae; Galliformes; Phasianida
                                                                                                                                       and assembly
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자
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red. No. 15;
Mismatches
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Pred.
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MEDLINE=95132616; PubMed=7831308;
Chang H.W., Li J., Kretzschmar D.,
                                                                                                                                          sequencing
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63
142
168
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431
47039 MR;
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                                                                                                                 Venter J.C.;
"Whole-genome random
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Euteleostomi; Homo.

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                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95322450; PubMed=7599184;

MEDLINE=95322450; PubMed=7599184;

Mises S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,

Mises S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,

Mises S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,

Mises S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,

Mises S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,

Mises S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,

Mises S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,

Mises S., Murphy D.B., Schlung A., Burfeind B., Schming Specificity (By Similarity).

Mises S., Murphy D.B., Schlung A., Burfeind B., Schming B., Schming Specificity (By Similarity).

Mises S., Murphy D.B., Schlung A., Burfeind B., Schming B., Sc
                                                                                                                                                                                                                                                                                                                                                        of the fork head gene family.";
                                                                                                                                                                                                                                                                                     Schmundt D., Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X78202; CAA55038.1; -.
EMBL; X74143; CAA52240.1; -.
EMBL; X74143; CAA52240.1; -.
FIRE, I37451; I37451.
HSSP; Q63245; 2HFH.
TRANSFAC; T02292; -.
Genew; HGNC:3811; FOXG1A.
MIM; 600779; -.
GO; GO:0003677; F:DNA binding; TAS.
GO; GO:0003677; F:DNA binding; TAS.
GO; GO:0003677; F:DNA binding; TAS.
InterPro; IPR001766; TF Fork head.
FroDom; PR001250; FORKHEAD.
FRINTS; PR001339; FORKHEAD.
FROSITE; PS00657; FORK HEAD.
FROSITE; PS00658; FORK HEAD.
FROSITE; FORK HEAD.
FROSITE FORK HEAD.
FROSITE FORK HEAD.
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                                               Craniata; Vertebrata; E
Catarrhini; Hominidae;
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red. No. 16;
Mismatches
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PRO-RICH.
POLY-GLN.
POLY-ARG.
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                                                                                                                                                                                                                                         MEDLINE=95048332; PubMed=7959731;
Murphy D.B., Wiese S., Burfeind P.,
Schulz-Schaeffer W., Thies U.;
"Human brain factor 1, a new member
Genomics 21:551-557(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
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50539 PW;
         Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                    FROM N.A.
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469
                                                                                                                                                                                SEQUENCE FROM
TISSUE=Brain;
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FXGE HUMAN
ID FXGE HUMAN
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Best Local S
Matches 7
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                                                                       P SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=White leghorn; TISSUE=Retina;

MEDLINE=96338226; PubMed=8757134;

Yuasa J., Hirano S., Yamagata M., Noda M.;

Transcription factors in the retina.*;

Nature 382:632-635(1966).

L Arranscription factors in the retina.*;

L Involution factors in the retina.*;

C -!- SUBCELLULAR LOCATION: Nuclear (Potential).

C -!- DEVELOPMENTAL STAGE: Can be detected in regions including

Drimordial retina and neuroepithelium by embryonic day 2 (E2). At

C -!- DEVELOPMENTAL STAGE: Can be detected in regions including

CC primordial retina and neuroepithelium by embryonic day 2 (E2). At

CC primordial retina and neuroepithelium and pigment epithelium as well

as in the telencephalon, and at E7 is expressed in retinal

CC disappear by E10.

CC -!- SIMILARITY: Contains 1 fork-head domain.

--- SIMILARITY: Contains 1 fork-head domain.

--- Tissum produced through a collaboration from the release of the collaboration from the coll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboraties wiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commentatives requires a license agreement (See http://www.isb-sib.ch/annousend an email to license@isb-sib.ch).
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EMBL; L36814; AAA66954.1; -
EMBL; U47275; AAB08466.1; -
PIR; A55909; A55909.
HSSP; Q63245; ZHFH.
TRANSFAC; T01833; -
InterPro; IPR001766; TF Fork head.
Prodom; PR0053; FORKHEAD.
Prodom; PR000425; TF Fork head; 1.
RMART; SM00339; FH; I.
PROSITE; PS00658; FORK HEAD 1; 1.
PROSITE; PS00658; FORK HEAD 2; 1.
PROSITE; PS00658; FORK HEAD 3; 1.
Transcription regulation; DNA-binding; Nuclear protein; DOWAIN 55 58 POLY-RIS.
DOWAIN 64 67 POLY-RIS.
DOWAIN 103 106 POLY-ALA.
COMMAIN 1142 233 FORK-HEAD.
SEQUENCE 451 AA; 48856 MW; E9B58407D2321B50 CRC64;
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PS5316;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Forkhead box protein G1A (Forkhead-related protein FXHL2)
(Transcription factor BF-2) (Brain factor 2) (BF2)
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         e qin oncogene."; 92:447-451(1995)
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RESULT 14
FXGA_HUMAN

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TISSUE=Brain;

MEDLINE=95322450; PubMed=7599184;

Miese S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,

Miese S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,

Miese S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,

Miese S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,

The genes family, are clustered on chromosome 14q.";

Biochim. Biophys. Acta 1262:105-112(1995).

C.-!- FUNCTION: Plays an important role in the establishment of the regional subdivision of the developing brain and in the development of the telencephalon. Sequence-specific DNA-binding protein with a distinct binding specificity (By similarity).

C.-!- SUBCELLUAR LOCATION: Nuclear.

C.-!- SUBCELLUAR LOCATION: Nuclear.

C.-!- SIMILARITY: Contains 1 fork-head domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the fork head gene
                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Forkhead box protein G1B (Forkhead-related protein FKHL1)
(Transcription factor BF-1) (Brain factor 1) (BF1) (HFK1)
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FORK-HEAD.
71CFD0BD069CFAD5 CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
NCBI TaxID=9606;
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HSSP, Q63245; 2HFH.
TRANSFAC; T02350; -.
Genew; HGNC:3812; FOXG1B.
MIM; 164874; -.
GO; GO:0003677; F:DNA binding; TAS.
GO; GO:0007420; P:brain development; TAS.
InterPro; IPR001766; TF Fork head.
From: PF00250; Fork head; 1.
PRINTS; PR00053; FH; I.
PROSITE; PS00657; FORK HEAD 1; 1.
PROSITE; PS00657; FORK HEAD 2; 1.
DOMAIN 33 57 HIS-RICH.
DOMAIN 33 57 HIS-RICH.
DOMAIN 72 75 POLY-LEU.
DOMAIN 168 259 FORK-HEAD.
SEQUENCE 477 AA; 51340 MW; 71CFD0BD069C
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Mismatches
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TISSUE=Brain;
MEDLINE=95048332; PubMed=7959731;
Murphy D.B., Wiese S., Burfeind P., ScSchulz-Schaeffer W., Thies U.;
"Fuman brain factor 1, a new member of Genomics 21:551-557{1994}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7
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PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:* 4004 Database :

283366

Total number of hits satisfying chosen parameters:

0

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Searched:

Post-processing: Listing first 45 summaries

seq length: 0 seq length: 2000000000

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ALIGNMENTS

RESULT 1 ANJOIG Glycocest and CP2310, renal - rat (fragments) Glycoprotein GP330, renal - rat (fragments) Clycosesion: Astus an corregions (Norway rat) Clycosesion: A3063 R. Accession: A3063 R. Raychowdhury, R.; Miles, U.; McCluskey, R.T.; Smith, J.A. Science 244, 1163-1165, 1989 R. Raychowdhury, R.; Miles, U.L.; McCluskey, R.T.; Smith, J.A. Science 244, 1163-1165, 1989 R. Raychowdhury, R.; Miles, U.L.; McCluskey, R.T.; Smith, J.A. A. Accession: A3053 A. Accession: A3053 A. Accession: A3053 A. Accession: A3053 A. Accession: A3054 A. Residues: 1-972 cRAy C. Superimally: alpha-2-macroglobulin receptor; EGP homology; LDL receptor ligand-binding repeat homology; LDLs receptor ligand-binding repeat homology cLDLs F. G. Superimalis: LDL receptor ligand-binding repeat homology cLDLs F. G. Superimalis: LDL receptor ligand-binding repeat homology cLDLs F. Residues: LDL receptor ligand-binding repeat homology cLDLs F. Residues: LDL receptor ligand-binding repeat homology cLDLs F. A55-238 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A55-238 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A55-469 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A55-469 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A55-469 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A55-469 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A55-469 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A79-551 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A79-551 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A79-551 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A79-551 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A79-551 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A79-551 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A79-551 (Domain: LDL receptor ligand-binding repeat homology cLDLs F. A79-551 (Domain: LDL receptor ligand-binding repeat homology cMB (DLS) F. A79-55	Oy 9 SGTCOPTOFRC 19
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beta-hydroxylase

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J. Biol. Chem. 265, 1029-1035, 1990

A; Title: Primary amino acid sequence of bovine dopamine beta-hydrox A; Reference number: A34926; MUID: 90110082; PMID: 2295597

A; Accession: A34926

A; Status: preliminary

A; Molecule type: protein

A; Residues: 33-55, RVV, 59-63; 73, 'F', 75-411; 420-441; 445-465; 468-559

R; Taylor, C.S.; Kent, U.M.; Fleming, P.J.

J. Biol. Chem. 264, 14-16, 1989

A; Title: The membrane-binding segment of dopamine beta-hydroxylase

A; Reference number: A31802; MUID: 89079641; PMID: 2909511

A; Molecule type: protein
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Residues: 33-37 <TAY>
Skotland, T.; Ljones, T.; Flatmark, T.; Sletten, K.
ochem. Biophys. Res. Commun. 74, 1483-1489, 1977
Title: NH-2-terminal sequence of dopamine beta-bydroxylase
Reference number: Al2853; MUID:77134133; PMID:843373
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ASJ860
Gopanine beta-moncoxygenase [EC 1.14.17.1] precursor, membrane-bound - h
Alerante names: dopanine beta-hydroxylase
C,Species: Dos prindgenius teaurus (cattle)
C,Dete: 0.9-Max-1990 #sequence revision of 0.7m.1995 #text change 05-Nov-1
C,Accession: AJ350, A34959. J30191; A3279; A41764 A34956; A31802; A37
E,Taljanidaz, J.; Streart, L.; Smith, A.J.; Klimman, J.P.
Biochemistry 28, 10054-10061, 1999
A)Aritle: Gtructure of bovine adrenal dopanine beta-moncoxygenase, as ded
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                     A; Title: Complete cloning and sequencing of rat gp330/megalin, a dis A; Reference number: A58173; MUID:95024033; PMID:7937880
A; Accession: T42737
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: 1-4660 <SAI>>
A; Residues: 1-4660 <SAI>>
A; Experimental source: strain Sprague-Dawley; kidney
C; Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL rec
F; 1-25/Domain: signal sequence #status predicted <SIG>F; 26-4660/Product: gp330 protein #status predicted <MAT>
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dopamine beta-hydroxylase
, PMID:2909511

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Diochem. Blophys. res. Commun. 7, 1401-1403, 137.

A) Accession: Al2853; MUID:77134133; PMID:64373

A) Accession: Al2863; MUID:77134133; PMID:64373

A) Accession: Al2863; MUID:77134133; PMID:643373

A) Accession: Al2863

A) Molecule type: protein

A) Residues: 33-34, T',36-44, X',46-47, TX',50 <8X0>

A) Molecule type: protein

A) Residues: 33-34, T',36-44, X',46-47, TX',50 <8X0>

A) Mole: residue 46 was also sequenced as Ile

R) Robertson, J.G.; Adams, G.W.; Medzihradszky, K.F.; Burlingame, A.L.; Villafranca, J.C.

Biochemistry 33, 11563-11575; 1994

A) Title: Complete assignment of disulfide bonds in bovine dopamine beta-hydroxylase.

A, Totle: Complete assignment of disulfide bonds in bovine dopamine beta-monoxygenase catalyzes the biosynthetic conversion of dopamir C; Comment: Dopamine beta-monoxygenase is a tetrameric glycoprotein bound in both the n C; Comment: Dopamine beta-monoxygenase is a tetrameric glycoprotein; monoxygenase is a tetrameric dopomine beta-monoxygenase is predicted <81G>
C; Superfamily: peptidyglycine monoxygenase; membrane-bound form #status predicted <MI F; 1-610/Product: dopamine beta-monoxygenase; membrane-bound form #status predicted <AN F; 1-610/Product: dopamine beta-monoxygenase; membrane-bound form #status predicted <AN F; 1-32/Domain: signal sequence #link MIS #status predicted <AN F; 1-32/Domain: signal sequence #link MiS #status predicted <AN F; 117, 559-604/Binding site: carbohydrate (Asn) {covalent}; fstatus experimental F; 223, 225-226/Binding site: copper (His) #status predicted <AN F; 233, 2405, 405, 407, 407, Pinding site: copper (His) #status predicted <AN F; 234, 2405, 407, 407, Pinding site: copper (His) #status predicted <AN F; 234, 239, 251, 252, 256/Binding site: copper (His) #status predicted <AN F; 231, 232, 251, 252, 256/Binding site: copper (His) #status predicted <AN F; 231, 232, 252, 256/Binding site: copper (His) #status predicted <AN F; 231, 232, 252, 256/Binding site: copper (His) #status predicted <AN F; 231, 232, 252, 256/Binding site: corper (His) #st
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Sekimizu,
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R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, S, Kuroda, M.; Ohta, T.; Tobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus in A; Reference number: A89758; MUID:21311952; PMID:11418146
A; Reference number: A89758; MUID:21311952; PMID:11418146
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-759 < KUR>
A; Cross-references: GB:BA000018; PID:g13701435; PIDN:BAB42729.1; GSPDB:CCC; Genetics:
A; Genetics:
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pue, R.; Kaito, C
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C;Accession: A69323
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dc.; Klenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L. Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arc A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: A69323
A;Accession: A69323
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-90 <KLE>
A;Cross-references: GB:AE001064; GB:AE000782; NID:92689387; PIDN:AAB90659.1; PID:926
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G97172
hypothetical protein CAC2213 [imported] - Clostridium acetob
C; Species: Clostridium acetobutylicum
C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_cha
C; Accession: G97172
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.
J; Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J; Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Sol
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97172
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-135 < XUR>
A;Cross-references: GB:AR001437; PIDN:AAK80170.1; PID:g15025
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2213
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); Mismatches
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Pred. No. 14;
0; Mismatches
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Pred. No. 13;
0; Mismatches
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Best Local Similarity
Matches 7; Conser
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C;Species: Homo sapiens (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21
C;Accession: T37190
R;Kestila, M.; Lenkkeri, U.; Mannikko, M.; Lamerdin, J.; McZready, ason, K.
Molecular Cell 1, 575-582, 1998
A;Title: Positionally cloned gene for a novel glomerular protein - A;Reference number: Z21629; MUID:98325371; PMID:9660941
A;Reference number: Z21629; MUID:98325371; PMID:9660941
A;Reference number: Z21629; MUID:98325371; PMID:9660941
A;Residues: I-1241 <KES>
A;Cross-references: EMBL:AFGS>
A;Cross-references: EMBL:AFGS>
A;Genetics:
A;Mote: mutated in congenital nephrotic syndrome of the Finnish ty
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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T26859
hypothetical protein Y43F8B.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_cha
C;Accession: T26859
R;Ainscough, R.
Submitted to the EMBL Data Library, October 1998
A;Reference number: Z20278
A;Reference number: Z20278
A;Reference number: Z20278
A;References: DNA
A;Residues: 1-1743 <WIL>
A;Residues: 1-1743 <WIL>
A;Cross-references: EMBL:AL032623; PIDN:CAA21511.1; CESP:Y43
A;Experimental source: clone Y43F8B
C;Genetics:
A;Gene: CESP:Y43F8B.3
A;Introns: 65/1; 92/2; 128/1; 229/1; 367/1; 422/1; 486/2; 52
                         Length
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Pred. No. 11;
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                       Score 8; DB 2;
Pred. No. 5.3;
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Matches 8; Conservative
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Best Local Similarity 100.
Matches 8, Conservative
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, T.; Tanaka, T.; Kuđoh, Y.; Yamazaki,
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                                                                                                                                    RESULT 12
S60198
glycine cleavage system protein H precursor (clone HFP13) - Flaveria pringlei (NiAternate names: H-prodein
C; Species: Flaveria pringlei
C; Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
C; Accession: S60198
R; Ropriva, S.; Bauwe, H.
Mol. Gen. Genet. 249, 111-116, 1995
A; Title: H-protein of glycine decarboxylase is encoded by multigene families in A; Reference number: S60194; MUID:96140454; PMID:8552027
A; Reference number: S60198
A; Status: nucleic acid sequence not shown; translation not shown
A; Residues: 1-161 < KOD>
A; Residues: 1-161 < KOD < K
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R; Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Woos submitted to the EMBL Data Library, September 1997

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Hamlin, N.; Holroyd
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C; Species: Myccbacterium leprae
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-:
C; Accession: D87019
R; Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; R; Cole, S.T.; Eiglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Ham; eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J. A; Title: Massive gene decay in the leprosy bacillus.
A; Reference number: A&6909; MUID:21128732; PMID:11234002
A; Residues: Dreliminary
A; Molecule type: DNA
A; Residues: 1-202 <STO>
A; Residues: 1-202 <STO>
A; Genetics:
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A; Genetics:
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C; Genetics:
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Pred. No. 20;
0; Mismatches
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Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
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125 DVFGLRR 131 \$

transposase BWEI1423 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: A13429
C;Accession: A13429
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltsman, E.; Selkov, B.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitene A;Reference number: AD3252; PMID:11756688
A;Reference number: AD3252; PMID:11756688
A;Reference number: AD3252; PMID:11756688
A;Residues: 1-217 <KUR>
A;Residues: 1-217 <KUR>
A;Residues: 1-217 <KUR>
A;Coss-references: GB:AE008917; PIDN:AAL52604.1; PID:g17983423; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1423
A;Map position: I

Gaps ö Indels Length ö Score 7; DB 2; Pred. No. 21; 0; Mismatches 3.4%; Sc. 100.0%; Pi Query Match Best Local Similarity 100. Matches 7; Conservative

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US-10-245-147-10
US-10-245-139-10
US-10-245-739-10
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US-10-245-185-10
US-10-245-185-10
US-10-245-143-10
US-10-245-143-10
US-10-245-845-10
US-10-238-346-10
US-10-238-346-10

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Quianjin, Hu
Garcia, Pablo
Williams, Lewis T.
Kothakota, Strinivas
TITLE OF INVENTION: Secreted Human Proteins
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Bmeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/935,390A
FILING DATE: 22-Aug-2001
CLASSIFICATION NUMBER: US/99935,390A
FILING DATE: 1997-12-11_ARGEST:
APPLICATION NUMBER: 08/988,671
FILING DATE: 1997-12-11_ARGEST:
APPLICATION NUMBER: 33,332
RIGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 1369.002
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                 Escobedo, Jaime
Quianjin, Hu
                                                                                                                                                                                   RESULT 1
US-09-935-390A-23
; Sequence 23, Application US/
; Patent No. US20020076761A1
; GENERAL INFORMATION:
APPLICANT: Escobedo,
Quianjin,
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                                                                                                                                 206;
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MIYAZAWA, Keiji
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
AND METHOD OF PRODUCING THE PROTEIN
                                                                                                                                                        Indels
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Pred. No. 8.5e-196;
0; Mismatches 0;
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e, N.W.
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/765,449

FILING DATE: 22-Jan-2001

PRIOR APPLICATION NUMBER: 08/685,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZINN, MA
Avenue,
INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 206 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. US20020076761A1e

SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-935-390A-23
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                                                                                                                                                                                                                                                                                                                           PTPASSTVSTTEDTEHLVYNHTTRPL
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ADDRESSEE: SUGHRUE, MION,
STREET: 2100 Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09765449
Patent No. US20020098537A1
GENERAL INFORMATION:
APPLICANT: SHIMOMURA, Takeshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                SHIMOMURA, Takeshi
KAWAGUCHI, Toshiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: <Unknown>
MATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
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SEQUENCE DESCRIPTION: SEQ
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11 Similarity 100.0%;
206; Conservative
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAWAGUCHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
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STRAIN: MR
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                                                            MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDBACEKYTSGFDELQRIH
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Pred. No. 5.3e-135;
0; Mismatches 0;
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0
Score 206; DB 9;
Pred. No. 1.9e-19;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09742201

Sequence 2, Application US/09742201

Patent No. US20020123091A1

GENERAL INFORMATION:

APPLICANT: Gurney, Austin L.

APPLICANT: Kirchhofer, Daniel K.

APPLICANT: Wood, William I.

TITLE OF INVENTION: No. US20020123091A1e1 Inhi

TITLE OF INVENTION: No. US20020123091A1e1 Inhi

FILE REFERENCE: P1861R1US

CURRENT APPLICATION NUMBER: US/09/742,201

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: PCT/US00/06884

PRIOR APPLICATION NUMBER: US 60/253,665

TYPE: PRI

CREANISM: HOMO Sapiens

TYPE: PRT

CREANISM: HOMO Sapiens
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Sequence 42, Application US/10081056
Publication No. US20040043927A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
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100.0%; Pr
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Query Match
Best Local Similarity 100.
Matches 206; Conservative
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US-09-742-201-2
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RESULT 5
US-10-245-752-10

Sequence 10, Application US/10245752

Sequence 10, Application US/10245752

Sequence 10, Application No. US2003064473A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Filvarcff, Bllen
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Scopy, Austin
APPLICANT: Scopy, Austin
APPLICANT: Print OF INVENTION: ACIDS ENCODING THE SAME
APPLICANT: PROS, Sherman
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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              PRIOR APPLICATION NUMBER: US 09/828,366
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR APPLICATION NUMBER: US 09/866,028
PRIOR APPLICATION NUMBER: US 09/866,028
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: PCT/US01/17443
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 383
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100.0%; Pr
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Matches 145; Conservative
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APPLICANT: Gerber, Hanspeter
APPLICANT: Gerles, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Hand, Semeth
APPLICANT: Hand, Semeth
APPLICANT: Milliams; Pan, Key
APPLICANT: Williams; Pan, Key
APPLICANTON WINDER: US 04, 742, 922
PRIOR PILLIAGO DATE: 2000-09-10-24
PRIOR PILLIAGO DATE: 2000-09-10-34
PRIOR PILLIAGO DATE
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R APPLICATION NUMBER: US 09
R FILING DATE: 2001-03-09
R APPLICATION NUMBER: US 09
R FILING DATE: 2001-03-14
R APPLICATION NUMBER: US 09
R FILING DATE: 2001-03-22
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APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Glovaroff, Ellen
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Fong, Sherman
APPLICANT: Wood, William
APPLICANT: Fong, Sherman
APPLICANT: Fong, 
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Pred. No. 5.3e-135
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                                                                                          PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-24
                       APPLICATION NUMBER: 60/065027
FILING DATE: 1997-11-10
APPLICATION NUMBER: 60/079689
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Matches 145; Conservative (
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APPLICANT: Aenkemazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Piti, Robert M.
APPLICANT: Suith, Victoria
APPLICANT: Suith, Victoria
APPLICANT: Some, Donna M.
APPLICANT: Matanabe, Colin K.
APPLICANT: Matanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE RITE OF INVENTION: COMPOSITIONS AND METHOR FILLING DATE: 1996-04-01
PRIOR FILLING DATE: 1996-04-01
PRIOR FILLING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: 60/059121
PRIOR FILLING DATE: 1997-10-17
PRIOR FILLING DATE: 1997-10-24
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PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removement of SEQ ID NO 10
LENGTH: 529
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100.0%; P:
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-10-245-859-10
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APPLICANT: Bater, Mean APPLICANT: Bater, Mean APPLICANT: Bater, Dan Goddard, Audrey APPLICANT: Grimaldi, J. Christopher APPLICANT: Grimaldi, J. Christopher APPLICANT: Gurney, Jaustin APPLICANT: Shiph, Victoria APPLICANT: Shiph, Victoria APPLICANT: Shiph, Victoria APPLICANT: Matanbe, Colin APPLICANT: Matanbe, Colin APPLICANT: Fong, Jemman APPLICANT: Jemman APPL
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Mismatches 0;
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                                                                                                                                                                                     Sequence 10, A
Publication No
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APPLICANT: Gerber, Hans-Peter
APPLICANT: Gerber, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Goddwaki, Paul J.
APPLICANT: Goddwaki, Paul J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Harsters, Scot A.
APPLICANT: Pan, J.
APPLICANT: Pan, J.
APPLICANT: Pan, J.
APPLICANT: Pan, J.
APPLICANT: Stephan, J-P F.
APPLICANT: Wood, W.I.
APPLICANT: Wood, W.I.
APPLICANT: Wood, W.I.
APPLICANT: Williams, P.M.
APPLICANT: Williams, P.M.
APPLICANT: Williams, P.M.
APPLICANT: Wood, W.I.
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5.3e-135;
                                                                                  File
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                                                                                    See
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Pred. No.
                                                                                                                                                                                                                                                                                              Score 145;
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 258
SEQ ID NO 12
LENGTH: 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145
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                                                                                                                                                                                                                                                                                                                             Pred
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Sequence 42, Application US/10305654
Publication No. US20030224984A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.4%; Sc.
100.0%; Pr
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Gerber, Hans-Peter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
Marsters, Scot A.
                                                                                                                                                                                                                                                                                                70.48;
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                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                   Homo sapiens

; TYPE: PRT
; ORGANISM: Homosapiens
US-10-305-654-42
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Best Local Similarity
Matches 145; Conser
                                                                                                                                                                                                                                                                                                                          il Similarity
145; Conser
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                                                                                                                                                                                   TYPE: PRT
ORGANISM:
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Best Local S
Matches 145
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US-10-3
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LENGTH: 529
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Best Local S
Matches 145
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ORGANISM:
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                                                                          APPLICANT: Baker, kevin.
APPLICANT: Baker, kevin.
APPLICANT: Baton, Dan
APPLICANT: Baton, Dan
APPLICANT: Goddard, Audrey
APPLICANT: Grinaldi, J. Christopher
APPLICANT: Grinaldi, J. Christopher
APPLICANT: Grinaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Mood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Pong, Sherman
APPLICANT: NWERR: 10/197942
FRICK RESERRACE: PS 5650RICTI
CURRENT APPLICATION NUMBER: US/10/245,107
CURRENT PILING DATE: 2002-07-16
FRIOR FILING DATE: 1997-09-16
FRIOR PLICATION NUMBER: 60/053046
FRIOR PLICATION NUMBER: 60/053046
FRIOR PLICATION NUMBER: 60/05699
FRIOR PLICATION NUMBER: 60/05699
FRIOR PLING DATE: 1998-03-27
FRIOR PLING DATE: 1998-03-27
FRIOR PLING DATE: 1998-06-18
FRIOR PLING DATE: 1998-06-24
FRIOR APPLICATION NUMBER: 60/08567
FRIOR PLING DATE: 1998-06-24
FRIOR FILING DATE: 1998-06-24
FRIOR FILING DATE: 1998-06-24
FRIOR FILING DATE: 1998-06-24
FRIOR APPLICATION NUMBER: 60/090557
FRIOR PLING DATE: 1998-06-24
FRIOR FILING DATE: 1998-06-24
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Pred. No. 5.3e-135;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 116
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. US20030068779A1
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100.0%; Py
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                   Sequence 10, Applicat
Publication No. US200
GENERAL INFORMATION:
APPLICANT: Baker, Kev
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145; Conser
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Best Local S
Matches 145
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-107
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Sequence 10, Application US/10245143 Publication No. US20030068780A1 GENERAL INFORMATION:

US-10-245-143-10

APPLICANT: Baker, Kevin APPLICANT: Eaton, Dan

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APPLICANT: Filvaroff.Ellen
APPLICANT: Gardard, Audrey
APPLICANT: Garney, Aug.in
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Pang, Semin
APPLICANT: Pang, Semi
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Pred. No. 5.3e-135;
0; Mismatches 0;
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; Publication No. US20030068781A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Smith, Victoria
; APPLICANT: Smith, Victoria
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RESULT 14
US-10-245-883-10
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APPLICANT: Watambe, Colin
APPLICANT: Watambe, Colin
APPLICANT: Wood, William
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
TITLE OF INVENTION: ACIDS ENCODING THE SAMB
FILE REFERENCE: P3630R1C98
CURRENT APPLICATION NUMBER: US/10/245,771
CURRENT APPLICATION NUMBER: US/10/197942
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1998-01-24
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-02
PRIOR PRILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/090689
PRIOR PRILING DATE: 1998-06-02
PRIOR PRILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/090689
PRIOR PRILING DATE: 1998-06-02
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JANT: Filvaroff, Ellen

JANT: Goddard, Audrey

JANT: Gormaldi, J. Christopher

JANT: Gurney, Austin

JANT: Smith, Victoria

JANT: Stephan, Jean-Phillippe

JANT: Watanbe, Colin

JANT: Wood, William

JANT: Zhang, Zemin

JANT: Zhang, Sherman

OF INVENTION: ACIDS ENCODING THE SAME
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Pred. No. 5.3e-135;
0; Mismatches 0;
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Sequence 10, Application US/10245851

Publication No. US20030068782A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Gorney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Ratanbe, Colin

APPLICANT: Watanbe, Colin

APPLICANT: Watanbe, Colin

APPLICANT: Watanbe, Colin

APPLICANT: Watanbe, Colin

APPLICANT: Zhang, Zemin
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100.0%; Pr
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; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-771-10
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APPLICANT: Barel, mevin

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Watanbe, Colin

APPLICANT: Wood, William

APPLICANT: Thang, Zemin

APPLICANT: Zhang, Zemin

APPLICANT: Applicant

APPLICANT: 
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Pred. No. 5.3e-13
J; Mismatches 0
                                                                       US/10/245,851
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FILE REFERENCE: P3630R1C93

CURRENT APPLICATION NUMBER: US/10/245,
CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-11-10

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-05-22

PRIOR FILING DATE: 1998-06-02

PRIOR FILING DATE: 1998-06-02

PRIOR FILING DATE: 1998-06-02

PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-25

REMAINING PRIOR APPLICATION NUMBER: 60/090689

PRIOR FILING DATE: 1998-06-25

REMAINING PRIOR APPLICATION NUMBER: 60/090689
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Publication No. US20030068783A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
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PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
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Matches 145; Conservative 0;
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CURRENT APPLICATION NUMBER: US/10/237,535

CURRENT PILING DATE: 2002-09-06

PRIOR PPLICATION NUMBER: 10/197942

PRIOR PPLICATION NUMBER: 60/063046

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 60/065027

PRIOR APPLICATION NUMBER: 60/065027
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Pred. No. 5.3e-135;
Dr Mismatches 0;
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
Zhang, Zemin
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Publication No. US20030073188A1
GENERAL INFORMATION:
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il Similarity 100.0%; P
145; Conservative 0;
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US-10-245-883-10
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Baton, Dan
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PRICOR APPLICATION NUMBER: 60/090619
PRICOR APPLICATION NUMBER: 60/090619
PRICOR PLING DATE: 1998-06-24
PRICOR PLING DATE: 1998-06-25
PRICOR PLING DATE: 1998-07-01
PRICOR PLING DATE: 1998-01-12
PRICOR PLING DATE: 1999-01-12
PRICOR APPLICATION NUMBER: 60/13572
PRICOR PLING DATE: 1999-03-11
PRICOR APPLICATION NUMBER: 60/13572
PRICOR PLING DATE: 1999-03-12
PRICOR APPLICATION NUMBER: 60/14473
PRICOR APPLICATION NUMBER: 60/14599
PRICOR APPLICATION NUMBER: 60/144790
PRICOR APPLICATION NUMBER: 60/14599
PRICOR APPLICATION NUMBER: 60/14599
PRICOR PLING DATE: 1999-06-22
PRICOR APPLICATION NUMBER: 60/14699
PRICOR PLING DATE: 1999-07-20
PRICOR APPLICATION NUMBER: 60/14699
PRICOR PLING DATE: 1999-07-20
PRICOR APPLICATION NUMBER: 60/14693
PRICOR AP
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APPLICATION NUMBER: 60/1 FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/1 rapb.

us-09-935-390a-23.oll

R APPLICATION NUMBER: 60/162506

R FILING DATE: 1999-10-29

R APPLICATION NUMBER: 60/170262

R APPLICATION NUMBER: 60/170262

R APPLICATION NUMBER: 60/170811

R APPLICATION NUMBER: 60/18021

R APPLICATION NUMBER: 60/19663

R APPLICATION NUMBER: 60/19663

R APPLICATION NUMBER: 60/19663

R APPLICATION NUMBER: 60/20636

R FILING DATE: 2000-04-25

R APPLICATION NUMBER: 60/20636

R FILING DATE: 2000-06-05

R APPLICATION NUMBER: 60/20636

R FILING DATE: 2000-09-01

R APPLICATION NUMBER: 60/266419

R FILING DATE: 2000-09-05

R FILING DATE: 2001-01-16

R APPLICATION NUMBER: 60/266421

R FILING DATE: 2001-01-26

R FILING DATE: 2001-02-09

R FILING DATE: 2001-01-26

R FILING DATE: 2001-01-16

R FILING DATE: 2001-02-09

R FILING DATE: 2001-01-26

R FILING DATE: 2001-03-09

R FILING DATE: 1999-03-12

R APPLICATION NUMBER: 09/403297

R FILING DATE: 1999-03-12

R APPLICATION NUMBER: 09/403291

R APPLICATION NUMBER: 09/403291

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ö Length 529; Query Match
70.4%; Score 145; DB 14; Best Local Similarity 100.0%; Pred. No. 5.3e-135; Matches 145; Conservative 0; Mismatches 0; R FILING DATE: 2001-03-09
R APPLICATION NUMBER: 09/872035
R FILING DATE: 2001-06-01
R APPLICATION NUMBER: 09/918585
R FILING DATE: 2001-03-06
R APPLICATION NUMBER: 09/924419
R FILING DATE: 2001-08-06
R FILING DATE: 2001-08-09
R FILING DATE: 2001-08-09
R FILING DATE: 2001-08-13
R APPLICATION NUMBER: 09/929404
R FILING DATE: 2001-08-16
R APPLICATION NUMBER: 09/941992
R FILING DATE: 2001-08-28
R FILING DATE: 2001-08-28
R FILING DATE: 2001-08-28
R FILING DATE: 2001-08-28
R FILING DATE: 2001-11-30
R APPLICATION NUMBER: 10/001054
R FILING DATE: 2001-11-30
R RPLICATION NUMBER: 10/081056
R APPLICATION NUMBER: 10/081056
R RILING DATE: 2002-02-20
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R RILING DATE: 2002-02-20
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Search completed: April 22, 2004, 10:32:27 Job time : 362 sece

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2004, 08:30:04; Search time 70 Seconds (without alignments) 831.497 Million cell updates/sec
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ALIGNMENTS

AAW636 ID A	RESULT 1 AAW63684 ID AAW63684 standard; protein; 206 AA.
XX:	AAW63684;
123	24-SEP-1998 (first entry)
18 i	Human secreted protein 4.
ž ž	ell proliferation; cytokine
X.	fferentiation, regene
3 5	chemotactic; haemostatic; thrombolytic; tumour inhibition; anti-inflammatory activity; biomarker.
8 ¤	Homo sapiens.
ğ	
EEE	Key Domain 68122 /note= "kunitz type serine protease inhibitor domain"
3 3 3	WO9825959-A2.
설문	18-JUN-1998.
X & :	11-DEC-1997; 97WO-US022787.
X E.	11-DEC-1996; 96US-0032757P.
X &	(CHIR) CHIRON CORP.
X II X	Escobedo J, Hu Q, Garcia P, Williams LT, Kothakota S;
§ # # # \$	WPI; 1998-348453/30. N-PSDB; AAV43604.
	olypeptides - having cytokine, cell prolif
4 4	differentiation, activin of innibin, tumour innibition of anti- inflammatory activities.
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z ×	Claim I; Page 52; /8pp; English.
ខ	a human secreted protein. The specification provi
ខ	ited protein sequences (AAW63681 to AAW63699)
႘	equences shown in AAV43601 to AAV43619. The invention provide
႘	dentifying a secreted polypept
88	microsomes. The secreted procesns can be used in assays to determine biological activities, such as cytokine, cell proliferation, or cellular
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N-PSDB; AAL46725

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differentiation activities, tissue growth or regeneration, activin or inhibin activity, chemotactic or chemokinetic activity, haemostatic or thrombolytic activity, receptor/ligand activity, tumour inhibition, or anti-inflammatory activity. The proteins can also be used as biomarkers, to identify tissues or cell types which express the proteins, or a stage-or disease-specific alteration in protein expression. They can be used in protein interaction assays, to identify ligands or binding proteins. Compounds which affect the biological activities of the secreted proteins or their ability to interact with specific ligands can be identified using the proteins in screening assays. The proteins and antibodies that using the proteins in screening assays. The proteins and antibodies that bind specifically to the protein can also be used to design diagnostic tests and therapeutic compositions for diseases which may be associated with altered expression of these proteins. Fusion proteins can be used to target other protein domains to cellular membrane or they can be secreted extracellularly
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The present invention provides the protein and coding sequences of four human protease associated proteins, designated HPRAP-1, HPRAP-2, HPRAP-3 and HPRAP-4. Human protease associated proteins are expressed in cancer and HPRAP-4. Human protease associated with inflammation and the immune disorders. The sequences can be used to diagnose, treat or prevent cell proliferative and immune disorders. The sequences can be used to diagnose, treat or prevent cell proliferative and immune disorders, including actinic prevent cell proliferative, alterosclerosis, atherosclerosis, begatis, portasis, primary coturnal haemoglobinuria, polycythaemia vera, portasis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, portasis, paroxysmal nocturnal haemoglobinuris, and alterosclerosis, antyloaning spondylitis, amyloidosis, anaemia, asthma, atherosclerosis, autolimmune haemolytic anaemia, autoimmune the proportic dermatitis, cholecystitis, contact dermatitis, autoimmune the approximation of action of dermaticis, dermatomyositis, diabetes mellitus, erythema nodosum, atrophic gastritis, diabetes mellitus, fetalis, erythema nodosum, atrophic gastritis, diabetes mellitus, hyporeachis, erythema nodosum, atrophic gastritis, diabetes mellitus, osteoporoseis, pancreatis, discesse, Hashimoto's thyroiditis, hyporeachis and traumatoid arthritis, scleroderma, Sjognen's syndrome, systemic lupus erythematosis, systemic spring and trauma. He present sequence is the HPRAP-2 protein. Note: The present sequence is the HPRAP-2 protein. Note: The present sequence is the berwent family equivalent this Derwent basic but was
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the present invention provides the protein and coding sequences of four human protease associated proteins, designated HPRAP-1, HPRAP-2, HPRAP-3 and HPRAP-4. Human protease associated proteins are expressed in cancer and immortalised cell lines and tissues associated with inflammation and the immune response, and so appear to play a role in cell proliferative and immune disorders, including actinic the immune disorders. The sequences can be used to diagnose, treat or prevent cell proliferative and immune disorders, including actinic keratosis, arteriosclerosis, atherosclerosis, burstis, cirrhosis, provent cell proliferative and immune disorders, including actinic keratosis, arteriosclerosis, atherosclerosis, and immune disorders, portassis, primary chrombocythaemia, AIDS, Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anaemia, asthma, atherosclerosis, autoimmune hemolytic anaemia, autoimmune thyroiditis, bronchitis, cholecysticis, contact dermatitis, cronn's grathma, atherosclerosis, autopic dermatitis, dermatomyositis, diabetes mellitus, chychicis, pronchitis, dermatomyositis, diabetes mellitus, erythema nodosum, atrophic gastritis, diabetes mellitus, coodpasture's syndrome, yndrome, multiple sclerosis, myocacdial or pericarderma, slogare's syndrome, myasthaemia gravis, myocacdial or pericarderma, slogare's syndrome, myasthaemia gravis, myocacdial or pericarderma, slogare's syndrome, myasthaemia pravis, systemic lupus erythematosis, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, werner syndrome, systemic anaphylaxis, systemic lupus erythematosis, systemic slogarished from this infections and trauma. The present sequence is the HPRAP-2 protein, which was used in a homology comparison in the exemplification of the present sequence is the HPRAP-2 protein, wiscustory in the present sequence was not obtainable from this
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The present sequence is an inhibitor of the protease activity of hepatocyte growth factor (HGF) activator (HGFA), which has a molecular weight of about 40 kD when determined by SDS-PAGE. The inhibitor, which was isolated from the human cancer cell line MKN45, can be used as an ir vivo or in vitro regulatory factor for HGF or HGFA. It can also be used to raise antibodies, useful in kinetic studies of the inhibitor, or as assay standards
                                                                                                                                             Inhibition; inhibitor; protease; hepatocyte; growth factor; activation; activation; activation; regulation; regulator; antibody; kinetic study; assay standard.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPSDKGHCVDLPDTGLCKBSIPRWYYNPPSEHCARFTYGGCYGNKNNFBBEQQCLESCRG
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Pred. No. 5.4e-198;
; Mismatches 0;
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          34
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PIPASSIVSTIEDIEHLVYNHITRPL
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                                                                                                                           activator
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Best Local Similarity 100.0%; P
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N-PSDB; AAT90038.
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RESULT
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                                                                                                                                                                                                                                                                   plasmin;
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se - inhibits protease activi
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(HGP) activator
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PTPASSTVSTTEDTEHLVYNHTTRPL
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                                                                                                                                                                                                                                                                   growth factor; HAI-1; prevention; protease
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N-PSDB; AAX02200.
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                                                                                                                                                                                                                                                                                                                           sapiens
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Best Local Sim
Matches 206;
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                                                                                                                                                                                                                                 Human HAI-1
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                                                                                                                                                                                                                                                                     Hepatocyte treatment;
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AAW926
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The present invention relates to the isolation of human protein

modification and maintenance molecules (PMMM), and the polynucleotide

sequences encoding them. A total of PMMM polypeptides (designated PMMM to are disclosed. The sequences of the invention are useful

c -1 to PMMM-40) are disclosed. The sequences of the invention are useful

c for diagnosing a condition or disease associated with the expression of generating an expression profile of a sample containing the generating an expression profile of a sample containing the polynucleotides. The disease or conditions associated with decreased polynucleotides. The disease or conditions associated with decreased expression or overexpression of PMMM are cell proliferation disorders

(e.g. cancer, atherosclerosis), neurological disorders (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS, allergies), developmental disorders (e.g. hypothyroidism, Cushing's syndrome), gastrointestinal or epithelial disorders, and infections. The syndrome) gastrointestinal or epithelial disorders, and infections or in for effectiveness as agonists or antagonists of the polypeptides, or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, atherosclerosis, or infections.
                                                                                                                                                                                                                                                                     Human; protein modification and maintenance molecule; PMMM; cancer; cell proliferation disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; allergy; inflammatory disorder; AIDS; developmental disorder; hypothyroidism; Cushing's syndrome; gastrointestinal disorder; epithelial disorder; infection; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; vulnerary; antiinflammatory; thyromimetic.
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Ein JA, Li JX;
son PM, Kable AE,
Jin P, Chien D;
                                                                                                                                                                                                                                             and maintenance molecule-23 (PMMM-23)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 263-264; 311pp; English
PTPASSTVSTTEDTEHLVYNHTTRPL
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2001US-0335703P.
2001US-0334145P.
2001US-0337451P.
2001US-0337451P.
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                                                                                                                                   standard; protein;
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N-PSDB; ACA92438.
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                                                                                                                                                                                                                                                    Human protein
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25-OCT-2001;
09-NOV-2001;
28-NOV-2001;
06-DEC-2001;
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polynucleotide and compounds that activity of the polypeptide.

PMMM polypeptides of the invention
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                                                               ő
                                                                                /note= "pancreatic trypsin inhibitor (Kunitz)
281. .287
/note= "N-muric"
                                                 487;
                                                                Indels
                                                 Length
                                                                                                                                                206
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                                               Score 157; DB 6; L. Pred. No. 8.3e-149; ); Mismatches 0;
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altering the expression of the target
specifically bind to, or modulate the
ABU92021-ABU92060 represent the human
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The present sequence is that of novel human immunomodulator PR0256 (UNQ223), as deduced from cDNA (see AAF30055) isolated from a placental tissue library. PR0256 (58 kDa, p1 6.22) shows sequence homology to human bissue library. PR0256 (58 kDa, p1 6.22) shows sequence homology to human protein, suggesting protease-inhibitor activity. The invention protein, suggesting protease-inhibitor activity. The invention of proteins (see AAF30050-62) encoding novel human PR0 proteins (see AAF30050-62) encoding novel human PR0 infiltration of inflammatory cells into a tissue of a mammal, stimulating or thancing an immune response to an antigen. Claimed compositions comprising a PR0 DOTYPEPIGE or increasing the proliferation of IT-1 lymphocytes in a mammal in response to an antigen. Claimed compositions comprising a PR0 DOTYPEPIGE or its antagonist have the opposite effect. A claimed method for treating an immune related disorder, such as a T cell disorder, involves administering a PR0 polypeptide, an agonist antibody or an antagonist antibody. The disorder is selected from a systemic lupus erythematosus, rheumatorial arthritis, osteoarthritis, cidopathic inflammatory myopathy, Sjogen's systemic sclerosis, diapetes mellitus, immune active hepatitis, autoimmune haemolytic anaemia, autoimmune thrombotytopania, thyroiditis, diabetes mellitus, immune active hepatitis, primary biliary cirrhosis, granulomatous colitis and crohm's diseases (such as multiple sclerosis), autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous finesase, (auto)immune-mediated skin diseases (such as bullous skin disease, (auto)immune-mediated skin diseases (such as bullous skin diseases (auto)immune-mediated skin diseases (such as bullous skin diseases (auto)immune-mediated skin diseases (such as bullous skin associated diseases), allergic diseases (such as agastive errementation associated diseases (such as graft related skin diseases) (all claimed agastic rejection and passociated diseases) (all claimed errors) and errors antibod
 .366
= "low density lipoprotein class A domain protein
                                                                    family
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Pitti RM, Tumas
                                                398. .441
/note= "pancreatic trypsin inhibitor (Kunitz)
protein motif"
422. .428
/note= "N-myristoylation site"
423. .429
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Marsters SA,
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Mark MR,
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/note= "*
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/note=
426. .4
/note=
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Wood WI;
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/note=
523. .5
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N-PSDB; AAF30055.
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Watanabe CK,
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AAU86133 standard; protein;
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                                                                                                                 443
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                                                                                                                                                                                                                                                       Human, PRO256 protein, cardiovascular, endothelial, angiogenic disorder, cardiac hypertrophy, trauma, cardiant, age-related macular degeneration, gene therapy, angiogenesis, protease activity, hepatocyte growth factor, peripheral vascular disease, hepatic, renal injury, nephrotropic, tumour, restinosis, tranquillizer, vulnerary, cytostatic, hepatotropic.
                                                                                                                                                                                                                                                                                                                                                                           activator
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|CLESCRG
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                                                                GTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGF
                                                                                                                                                                                                                                                                                                                                                                          "Human mature hepatocyte growth factor
                                 529;
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                                 Length
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                           DB 4; rv
. le-136;
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/note= "N-myristoylation site"
282. .288
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e= "Asn is N-glycosylated"
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235. .239
/note= "Asn is N-glycosylated"
278. .298
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= "N-myristoylation
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                                Score 145;
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/label= Signal_peptide
29. .35
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                         70.4%; Sc.
100.0%; P;
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57
50
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310.
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/note= ""
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161. .167
/note= "N
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/note= "H
                                       Local Similarity 100.
 PR0256
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212. ?
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/note=
285. .2
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/note=
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lymphocytes using
                 529 AA;
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                Sequence
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Matches
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The present invention relates to PRO256 or its agonist/antagonist may be used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, especially a human with cardiac hypertrophy, trauma, a type of tumour or age-related macular degeneration. PRO256 may be administered together with a cardiovascular, endothelial, or angiogenic agent, a chemotherapeutic agent, a growth inhibitory agent, or a cytotoxic agent. PRO256 may also be used to treat the disorders above, preferably through administration via ex vivo gene therapy. PRO256 or its agonist may be used to inhibit endothelial cell growth, angiogenesis or protease activity of a hepatocyte growth factor. Stimulation or protease activity of a hepatocyte growth factor. Stimulation or inhibition of the protease activity of a hepatocyte growth factor. Stimulation or inhibition of the protease activity of a hepatocyte growth factor is preferably carried out where a mammal has a cardiovascular, endothelial, or angiogenic disorder selected from peripheral vascular disease, hepatic or renal injury or a restinosis disorder. The present sequence is human hepatocyte growth factor activator inhibitor, PRO256
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Pred. No. 1e-136;
0; Mismatches 0;
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                                       "M-myristoylation site"
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422. .428
/note= "N-myristoylation 8:
423. .429
/note= "N-myristoylation 8:
426. .432
/note= "N-myristoylation 8:
466. .483
/label= Transmembrane_domai
523. .527
/note= "Asn is N-glycosylat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-2000; 2000WO-US003565.
15-MAR-2000; 2000WO-US006884.
28-NOV-2000; 2000US-0253665P.
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N-PSDB; AAD16721.
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Homo sapiens
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                 384
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ABB8483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. AAU86128-AAU86162 represent the human PRO polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating
                                                            Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder;
inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillan KJ
Stone DM;
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Smith
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Pred. No. 1e-136
); Mismatches
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Pitti RM, Roy MA,
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99US-0123972P.
99US-0133459P.
99WS-0140650P.
99US-0144758P.
99US-0144758P.
99US-0145698P.
99US-014569P.
99WS-014569P.
99WO-US021090.
99WO-US028313.
99WO-US028313.
99WO-US028313.
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Best Local Similarity 100.0%
Matches 145; Conservative
                                                    polypeptide
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WOOG WI;
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N-PSDB; ABK40259.
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C.K.,
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inflammatory,
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11-MAY-1999;
02-JUN-1999;
22-JUN-1999;
20-JUL-1999;
26-JUL-1999;
26-JUL-1999;
28-JUL-1999;
31-AUG-1999;
17-AUG-1999;
01-SEP-1999;
01-DEC-1999;
01-DEC-1999;
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Marsters S
Watanabe C
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Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
                        44
protein sequence SEQ ID NO:42
                                              14
                                              529
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2000US-0220624P.
2000US-0220664P.
2000US-0220664P.
2000US-0222695P.
2000US-0222695P.
2000US-0222695P.
2000US-0222695P.
2000US-0230978P.
2000US-0230978P.
2000US-0242922P.
2000US-0242922P.
2000US-0242922P.
2000US-00665350.
2000US-00709238.
2000US-00709238.
2000US-00709238.
2000US-00709656.
2000US-00706520.
2001US-00706666.
2001US-00808689.
2001US-00808689.
2001US-00808689.
2001US-00854208.
2001US-00854208.
2001US-00854208.
2001US-00854208.
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2001US-00854208.
2001US-00854208.
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28-JUL-2000;
28-JUL-2000;
02-AUG-2000;
17-AUG-2000;
24-AUG-2000;
07-SEP-2000;
18-SEP-2000;
18-SEP-2000;
18-SEP-2000;
10-NOV-2000;
24-OCT-2000;
24-OCT-2000;
26-NOV-2000;
26-NOV-2000;
27-JAN-2001;
28-FEB-2001;
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ABEB8072 to ABEB8258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
activities, and can be used in gene therapy. The PRO polynucleotides,
proteins, agonists and antagonists are useful for treating or diagnosing
a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
angiogenesis (such as breast carcinoma and liver carcinoma) and wound
healing. The PRO polynucleotides have applications in molecular biology,
including use as hybridisation probes, and in chromosome and gene
mapping. ABL88259 to ABL88267 represent primers and probes used in the
cemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                          383
                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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a mammal.
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             Goddard A;
                                                                                                                                                                                                                                                                                                                                            Length 529;
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                       Pan Ye W;
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                                                                                     One hundred and eighty seven nucleic acids encoding PRO useful in diagnosis and treatment of cardiovascular (e.ginfarction), endothelial or angiogenic disorders in a ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted protein; transmembrane protein;
                       SA,
          Gerritsen ME, G
KJ, Marsters SA,
ms PM, Wood WI,
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le-136;
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Pred. No.
                   Hillan KJ, M
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                                                                                                                                 English.
            Gerber H,
                                                                                                                                                                                                                                                                                                                                   70.4%; SC.
100.0%; Pi
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2000US-0230621P.
2000US-0235147P.
2000WO-US030873.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein;
                      4. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                               565pp;
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         r KP, Ferrard
wski PJ, Gurney Al
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                                                      02-090516/12
ABL88092.
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145; Conser
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                                                                                                                                                                                                                                                                                                                     529 AA;
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                                                                                                                                 Claim 11; Fig
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05-SEP-2000;
22-SEP-2000;
10-NOV-2000;
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                               Stephan JF,
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                                                      2002
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                      Godowski
                                                    WPI; 200
N-PSDB;
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This invention relates to the cDNA and protein sequences of novel
secreted and transmembrane polypeptides PRO polypeptides. The invention
also comprises a method for producing the proteins of the invention by
recombinant means and antibodies specific for the protein of the
invention. The antibody may be used for detecting the PRO proteins of the
invention and may be used to modify their activity. Polynucleotides may
be used as hybridisation probes for a CDNA library to isolate the full-
length PRO cDNA or to isolate other cDNAs, to construct hybridisation
probes for mapping the gene which encodes that PRO and for genetic
analysis of individuals with genetic disorders, in assays to identify
other proteins or molecules involved in binding reaction, to generate
transgenic animals or knock-out animals which in turn are useful in the
development and screening of therapeutically useful reagents, for
chromosome identification, and tissue typing. The PRO polypeptides are
useful in gene therapy, and as molecular weight markers for protein
electrophoresis purposes. The sequence may also be used to detect
overexpression on PRO polypeptides in cancerous tumours and for screening
for differentially expressed genes using microarray technology. The
present sequence represents a human PRO protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           New PRO polypeptides and polynucleotides encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or genetic analysis of individuals with genetic disorders.
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Wood WI, Zhang
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Pred, No. 1e-136;
0; Mismatches 0;
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Stephan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 10; 218pp; English
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2001US-0261878P.
2001US-0261939P.
2001US-0264395P.
2001US-0264395P.
2001US-0264395P.
2001US-0264395P.
2001US-0264395P.
2001US-0264395P.
2001US-0264395P.
2001US-0280982P.
2001US-0282129P.
2001US-0282129P.
2001US-0282129P.
2001WO-US017800.
2001WO-US017862.
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                                                                                                                                                                                                                                                                                                                                               Saton DL,
Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-362426/39.
N-PSDB; ABK69965.
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Best Local Similarity
Matches 145; Conser
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12-JAN-2001;
16-JAN-2001;
16-JAN-2001;
25-JAN-2001;
02-FEB-2001;
09-FEB-2001;
09-MAR-2001;
04-APR-2001;
04-APR-2001;
04-APR-2001;
04-APR-2001;
04-APR-2001;
04-APR-2001;
05-MAY-2001;
25-MAY-2001;
29-JUN-2001;
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Fong S;
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Human PRO polypeptide
                                  Watanabe
                     Ferrara N,
(WILL/) WILLIAMS P M (WOOD/) WOOD W I.
                                               WPI; 2002-171999/22
N-PSDB; ABL95581.
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29-AUG-2001;
18-JUL-2002;
                  KP,
PJ,
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                                  Stephan JF,
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Best Local S
Matches 145
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                            Godowski
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                                                                      cancer;
dimorder;
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                                                                   Human; angiogenesis; PRO protein; cardiovascularisation; wound; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiantiarteriosclerotic.
                                                         ID NO:
                                                         SEQ
                                                       protein PRO256
                standard; protein; 529 AA
                                                                                                                                                            2000US-0219556P.
2000US-0220664P.
2000US-022664P.
2000US-022695P.
2000US-0222695P.
2000US-0222695P.
2000US-0222695P.
2000US-0230978P.
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BAKER K P.
FERRARA N.
GERBER H.
GERRITSEN
GODDARD A.
                                                         angiogenesis
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HILLAN K
MARSTERS
PAN J.
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STEPHAN J
WATANABE
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25-JUL-2000;
28-JUL-2000;
28-JUL-2000;
17-AUG-2000;
23-AUG-2000;
24-AUG-2000;
18-SEP-2000;
18-SEP-2000;
18-SEP-2000;
01-DEC-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
10-NOV-2000;
10-NOV-2000;
10-NOV-2000;
10-NOV-2000;
22-JAN-2001;
22-JAN-2001;
22-JAN-2001;
22-MAR-2001;
22-MAR-2001;
25-MAY-2001;
25-MAY-2001;
30-MAY-2001;
30-MAY-2001;
                                                                                                                       WO200208284-A2
                                                                                                                                                 -JUL-2001;
                                                                                                         Homo sapiens
                                            19-JUL-2002
                                                                                                                                    31-JAN-2002
   RESULT 12
ABB95443
ID ABB95443
                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH)
(BAKE/)
(FERR/)
(GERB/)
(GODD/)
(GODD/)
(GURN/)
(HILL/)
(MARS/)
(PAON/)
(STEP/)
(WATA/)
                              ABB95443
                                                          Human
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120
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                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention
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                  Paoni
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                  SA,
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Gerritsen ME,
KJ, Marsters S
ms PM, Wood WI
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Pred. No. 1e-136;
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 Gerber H, Gerri
, Hillan KJ, M
K, Williams PM,
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                                                                                                                                                                                                                                          Claim 11, Fig 42; 567pp; English.
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100.0%; P)
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2001WO-US027099.
2002US-00197942.
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Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for stimulating proliferation of human microvascular endothelial cells, and PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
            Grimaldi J
Wood WI,
            Goddard A,
Watanabe CK,
             ы
             Filvaroff E
Stephan JP,
(GETH ) GENENTECH INC
             Eaton DL,
Smith V,
                                       WPI; 2003-625484/59
N-PSDB; ADA01277.
             Baker KP,
Gurney AL,
                           Fong S;
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JC; Zhang

Claim 11; Fig 10; 307pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNP-alpha) from human blood, a method for stimulating the proliferation of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and lnn gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or medicament for tracting a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cells tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polypeptide of the invention.

529 AA; Sequence

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|CLESCRG
                                           MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACBKYTSGFDELQRIH
                           Ö
                                                                                PSSDKGHCVDLPOTGLCKESIPRWYYNPFSEHCARFTYGGCYGNKNNFEBEQO
        Length 529;
                          Indels
       Score 145; DB 6; 1
Pred. No. 1e-136;
0; Mismatches 0;
                                                                                                                       ISKNOVFCLRREIPIPSTGSVEMAV 145
                                                                                                                              70.4%; Sc.
100.0%; Pr
               il Similarity 100
145; Conservative
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       Query Match
Best Local
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               Best Loc
Matches
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Human; PRO; secreted protein; transmembrane protein; endothelial cell tube formation; chondrocyte cell differentiation; microvascular endothelial cell; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; kidney tumour; liver tumour; cytostatic; vaccine.
                                                                                                                                  Human secreted/transmembrane polypeptide PRO256
                              standard; protein;
                                                                                                (first entry)
                                                                                                20-NOV-2003
                                ADA43707
RESULT
              ADA43
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443

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The invention relates to an isolated secreted/transmembrane (PRO) polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid motecule selected from any one of the mucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO in specification, or a sequence having at least 80% identity to PRO in specification, or a sequence having at least 80% identity to PRO in without its associated signal peptide. An extracellular domain of PRO with or without its associated signal peptide, an extracellular domain of PRO, PRO, PRO (Esion proteins, inducing endothelial cell tube formation (by administering PRO281, PRO21807, PRO2893) or PRO3189, PRO4499, PRO6308, PRO6000, PRO10775, PRO21807, PRO21807, PRO21807, PRO50893 or PRO3189, PRO4499, PRO6308, PRO6000, PRO10775, PRO50801, PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPSDKGHCVDLPDTGLCKESIPRWYYNPPSEHCARFTYGGCYGNKNNFEEEQQCLESCRG
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                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 PRO21383, useful in molecular biology, chromosome and gene mapping, generating antisense RNA and DNA, and in gene therapy.
                                                                                                                                                                                                                                                          JC;
Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated secreted/transmembrane (PRO)
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Wood WI,
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Pred, No. 1e-136;
Pred, No. 1e-136;
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Watanabe CK,
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Stephan JP,
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larity 100.0%;
Conservative C
                                                                                                                      2002US-00245859
                                                                                                                                                              2001WO-US027099
2002US-00197942
                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                Eaton DL,
Smith V,
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N-PSDB; ADA43706,
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PRO21383 useful for stimulating the proliferation or differentiation
chondrocyte cells and detecting the presence of a tumor in a mammal
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                                                                                                   Human; PRO; secreted protein; transmembrane protein; endothelial cell tube formation; chondrocyte cell differentiation; microvascular endothelial cell; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; kidney tumour; liver tumour; cytostatic; vaccine.
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oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences, for measuring or detecting the expression of an associated gene, and as antisense probes. PRO nucleic acid is useful as hybridisation probe, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence represents a PRO protein.
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ALIGNMENTS

RESULT 1 BX334952/c LOCUS DEFINITION ACCESSION	BX334952 BX334952 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI009YC11 3-PRIME, mRNA sequence.
VERSION KEYWORDS SOURCE ORGANISM	BX334952.1 GI:30310380 BST. Homo sapiens (human)
RRFRRNCE	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 1201)
AUTHORS TITLE	Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unushished (2001)
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France
	Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7854.f For
	<pre>more intormation about this craster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DI009AB06NP1&cluster=7854.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600</pre>

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208

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148

1406

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1346

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BX382616 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI083YF21 3-PRIME, mRNA sequence.
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BX382616.1 GI:30439963
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Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI083CC11NP1&cluster=7854.f. Contact :
Feng Liang BRail : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI083CC11NP1.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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4; Mismatches 15;
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digested with Not I and cloned into the Not I and EcoR V
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      a
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Location/Qualifiers
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Best Local Similarity 97.1%;
Matches 1115; Conservative
       Avenue
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o sapiens F 70YA20 3-PR 70YA20 3-PR GI:30378436 (human) etazoa; Chc theria; Pri to 1073) to 1073) ber, C., Jes cDNA librar (2001) oscope Centre Nati	edex - France scope.cns.fr, Web : ww icted by Life Technolo equence belongs to sequence this cluster, see oe.cns.fr/ i?seq=CSODIO70BA10NP1& fliang@lifetech.com U invitrogen.com/ Invitroscope sequence ID : C halifiers ""Homo sapiens"	9606" YA20" ACENTA COT 25-NORMALIZED" Gapiens PLACENTA COT 25-NORMALIZED" Id cDNA was primed with a NotI-oligo(dT) me end enriched, double-strand cDNA was It I and cloned into the Not I and EcoR V INSPORT 6 vector. Library was normalized. Te 961.2; DB 13; Length 1073; The 961.2; DB 13; Length 1073;	403 AGGAGACATCCGGCGCTGGTACTA 1032 AAGAGAGCATCCCGCGCCT-GTACTA 463 ATGGTGGTTGTTACGGCAACAAGAA 463 ATGGTGGTTGTTACGGCAACAAGAA 523 GTCGCGGCATCTCCCAAGAAGGATGT 523 GTCGCGGCATCTCCCAAGAAGGATGT 6116	
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Homo sapies Homo sapies

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheleosto

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Bomo.

I (bases 1 to 1192)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7854.fr

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI070CE12NP1&cluster=7854.f. Contac

Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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BX381856 Homo sapiens PLACENTA COT 25-NORMALIZED Homo clone CS0DI070YJ23 3-PRIME, mRNA sequence.
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                      /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="CSODIG707J23"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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larity 93.9%; Pred. No. 1.6e-152;
Conservative 25; Mismatches 27;
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

L. (bases 1 to 1026)

S. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgiseq=cSiAI015ZAD4NP1&cluster=7854.f. Contact ;
Feng Liang Email : fliang@lifetech.com URL :
http://tullength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSIAI015ZAD4NP1.

Location/Qualifiers

Location/Qualifiers
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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1005 ACCCCTTCAGCGAACAC-GCSCCCGCTTTACCTATGKT-GTTGTTACGGCAACAAGAACA
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Pred. No. 4.3e-151;
4; Mismatches 3;
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Best Local Similarity 98.9%;
Matches 996; Conservative
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RESULT 6
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Homo sapiens

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

B 1 (bases 1 to 1201)

S Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

L Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12873845.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7854.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSOBE008CB03QPI&cluster=7854.f. Contact:

Feng Liang Email: iflangalifetech.com URL:

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID: CSOBE008CB03QPI.

Location/QualifierB
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ALS42118 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE008YD05
5-PRIME, mRNA sequence.
ALS42118
ALS42118.2 GI:30546953
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with a NotI-oliage (dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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7; Mismatches 34;
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BX340192 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI083YH19 3-PRIME, mRNA sequence.

BX340192

BX340192.1 GI:30341878
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was primer. Five prime end enriched into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BRail: Beqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This Bequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI083CDI0NP1&cluster=7854.f. Contact:
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI083CDI0NP1.
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Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 974)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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3; Mismatches 8;
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1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO75YN13"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.
                     Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
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Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

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primer, Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 1138)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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BX338259 Homo sapiens PLACENTA COT 25-NORM clone CS0DI057YA06 3-PRIME, mRNA sequence.
BX338259
BX338259.1 GI:30345682
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Homo sapiens (human)

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

S Li, W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

In Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Inhrary was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7854.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODI014CF02NP1&cluster=7854.f. Contact:

Feng Liang Email: fliang@lifetech.com URL:

Feng Liang Email: fliang@lifetech.com (InvitroGen Corporation 1600)

Faraday Avenue Genoscope sequence ID: CSODI014CF02NP1.

Location/Qualifiers

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BX335408 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens clone CS0DI014YL03 3-PRIME, mRNA sequence.
BX335408
BX335408.1 GI:30310424
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CTGGTACTACAACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTACGG 239 61 299 121 359 419 241 181 Query Match Best Local 1378 1318 71 DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE JOURNAL RESULT 13 BX336602 FEATURES COMMENT Ω A ይ ਨੇ හි ò В ठे Ś 1197 1257 1017 1077 1137 8 252 192 372 837 552 957 492 598 658 718 732 777 672 897 910 792 479 538 851 970 /organism="Homo sapiens"
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized. CCAGACT ||||||| |CCAGACT CACACCA GCTGCCTGTCCCTACCCCATGGTGCTAGGAAGAGGAGTGGGGGTGGTGTCAGACCCTGGAG CCACCCC | | | | | | | | | CCACCCC CTTGCCA ||||||||| |CTTGCCA CAGGCCC CTCACGT GTTACTG Trecece TGTGGCA GTTCAAA CTCACGT CAGGCCC AACAAGAACAACTTTGAGGAAGAGCAGCAGTGCC-TCGAGTCTTGTCGCGGCATCTCCAA CCTGAGAAAGCTCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGCCAGAAGTA TGGGTGAAGAGGGGAAGAGGCCTGTTTGGCCTCTCTATCCTCTTTCCTC 1068, ö Length Indels 13; Score 898.4; DB 13; Pred. No. 6e-142; 11; Mismatches 12; 11; ch 1 Similarity 97.0%; 987; Conservative 1198 1018 1078 1138 311 251 1258 551 Query Match Best Local S Matches 987 611 B 9 8 958 491 431 371 77B 671 838 969 850 791 719 731 1028 599 50 480 539 909 8 셤 2 ይ ਠੇ 셤 움 ç ઠે 원 g 셤 ઠે ò 윱 ò Ş ò å 뒩 ð ठ ô δ

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

B 1 (bases 1 to 1201)
S Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Upublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - Prance
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
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Library Was Genoscope sequence ID: CSODIO30AC12QPI. BX336602
BX336602 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI030YB23 5-PRIME, mRNA sequence.
BX336602
BX336602.1 GI:30339518
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized. 143 GGCTGCCTGTGAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAG CTGCATCGACAGTTTCCTGGAGTGTGACGACACCCCCAACTGCCCCGACGCCTCCGACGA 318 AAGATTGAGCTCTCTGCCCTTGATCAGCCCCACCCTGGCCTAGACCAGCAGAGAGCAA
131 AAGATTGAGCTCTCTGCTCTTGATCAGCCCCACCCTGGCCTAGACCAGCAAGAGCCA CAACATCACAGCC GGAGAAGCTCAGCTGCATTCCGCAGCCCCCCCCCAAGGTTCTCCAACATCACAGCCCAGCCCAAGAAGGTTCTCCAACATCACAGCCCAGCCCCAAGGTTCTCCAACATCAGCCCCCAAGG-TCTCCAACATCAGGCCCC Length 1201; 15, Indels ch 59.7%; Score 898.2; DB 13; Il Similarity 90.2%; Pred. No. 6.3e-142; 980; Conservative 32; Mismatches 60; I Homo sapiens (human) Homo sapiens

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672 612 899 g 셤 ઠે 01-JUN-2003 sapiens cDNA AL579407
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AL579407
Homo sapiens T CELLS (JURKAT CELL LINE) Homo sclone CS0DH004YB13 3-PRIME, mRNA sequence.
AL579407
AL579407
AL579407.2 GI:31317691
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut

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Library was not normalized."
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:12944423.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BRmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

7854.f For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DH004CA07NP1&cluster=7854.f. Contact:

Feng Liang Bmail: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID: CS0DH004CA07NP1.
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59.4%; Score 894.4; DB 9;

Best Local Similarity 90.6%; Pred. No. 2.7e-141;

Matches 931; Conservative 45; Mismatches 48;
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On Feb 16, 2001 this sequence version replaced gi:12933383.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7854.f

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODIO55AB08NP1&cluster=7854.f. Cont

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InvitroGen Corporation 160

Faraday Avenue Genoscope sequence ID : CSODIO55AB08NP1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                            AGATTGAGCTCTCTGCCCTTGATCAGCCCCACCCTGGCCTAGACCAGCAGACA
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Homo sapiens PLACENTA COT 25-NORMALIZED Homo sclone CS0DI055YC15 3-PRIME, mRNA sequence.
AL573797
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AL573797.2 GI:31295133
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Search completed: April 22, 2004, 08:09:57 Job time : 4182 secs

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US-10-245-055-9

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                                                                                                                  APPLICANT: Escobedo, Jaime

Quianjin, Hu

Quianjin, Hu

Garcia, Pablo

Williams, Lewis T.

Kothakota, Srinivas

TITE OF INVENTION: Secreted Human Proteins
NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA

COUNTRY: USA

ZIP: 94608-2916

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.(
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/935,390A
FILING DATE: 22-Aug-2001
CLASSIFICATION NUMBER: 08/986,571
FILING DATE: 1997-12-11
ATTORNEY/AGENT INFORMATION:
RECISTAATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 1369.002
TELECOMMUNICATION INFORMATION:
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RESULT 1
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; Sequence 4, Application US/09935390A
; Patent No. US20020076761A1.
; GENERAL INFORMATION:
; APPLICANT: Escobedo, Jaime
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TELERA: (510) 655-35-
TELEX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pai
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ
US-09-935-390A-4
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Best Local Similarity 100.0%;
Matches 1505; Conservative
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                 US-09-742-201-1

US-09-742-201-1

Sequence 1, Application US/09742201

Patent No. US20020123091A1

GENERAL INFORMATION:

APPLICANT: Gurney, Austin L.

APPLICANT: Kirchhofer, Daniel K.

APPLICANT: Kirchhofer, Daniel K.

APPLICANT: Wood, William I.

TITLE OF INVENTION: No. US20020123091A1el Inhi

TITLE OF INVENTION: for Use in Modulation of

FILE REFERENCE: P1861R1US

CURRENT APPLICATION NUMBER: US/09/742,201

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: PCT/US00/06884

PRIOR FILING DATE: 2000-03-15

PRIOR APPLICATION NUMBER: US 60/253,665

PRIOR PILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 6
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; LENGTH: 2482 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-742-201-1

EQ ID NO 1 LENGTH: 2482

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1388 2374 1208 1268 2254 1328 2434 2194 2074 rtgatcagccccaccctggcctagaccagcagacagagccaggagagctca ABCTCCTCTTCCATGCTGTGCGCCCAGGGCTGGGAGGAGGACTTCCCTGT Meilan

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NEATMENT OF DISORDERS INVOLVING ANGIOGENESIS

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ION NUMBER: US/10/081,056

ATE: 2002-02-20

N NUMBER: PCT/US01/21735

E: 2001-07-09

N NUMBER: US 60/220,624

E: 2000-07-25

N NUMBER: US 60/220,664

E: 2000-07-25

N NUMBER: US 60/220,664

E: 2000-07-28

N NUMBER: US 60/220,664

E: 2000-07-28

N NUMBER: US 60/222,695

N NUMBER: US 09/643,657

E: 2000-08-17

E: 2000-08-17 Dr. d, Audrey
ki, Paul J.
Austin L.
Kenneth J.
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Pred. No. 0;
0; Mismatches
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DR FILING DATE: 2000-11-08

R FILING DATE: 2000-11-08

DR APPLICATION NUMBER: PCT/US00/30952

DR FILING DATE: 2000-11-01

DR APPLICATION NUMBER: PCT/US00/32678

DR FILING DATE: 2000-12-01

DR FILING DATE: 2000-12-01

DR FILING DATE: 2000-12-20

DR FILING DATE: 2000-12-20

DR FILING DATE: 2000-12-20

DR FILING DATE: 2000-12-20

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DR FILING DATE: 2001-05-10

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FILING DATE: 2001-06-28
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Best Local Similarity 99.3%;
Matches 1474; Conservative
                Sapien
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; ORGANISM: Homo
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APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
Goddard, Austin
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanbe, Colin
APPLICANT: Dilyon NUMBER: US/10/245, 752
CURRENT FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-26
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PRIOR APPLICATION NUMBER: 60/090689
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090689
PRIOR P
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Publication No. US20030064473A1
GENERAL INFORMATION:
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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed -; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-859-9

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Best Local Similarity 99.3%
Matches 1474; Conservative
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APPLICAMY: Bator, Dan
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APPLICAMY: Filvaroff, Ellen
APPLICAMY: Goddard, Audrey
APPLICAMY: Goddard, Audrey
APPLICAMY: Goddard, Justin
APPLICAMY: Grimaldi, J. Christopher
APPLICAMY: Swith, Victoria
APPLICAMY: Smith, Victoria
APPLICAMY: Watanba, Jean-Phillippe
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APPLICAMY: SCRETED AND TRANSYEMBRANE POLYBEPTIDES AND NUCE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: US/10/245, 859
CURRENT APPLICATION NUMBER: 00/053114
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1999-03-27
PRIOR FILING DATE: 1999-03-27
PRIOR FILING DATE: 1999-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
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Sequence 9, Application US/10245859
Publication No. US20030064474A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/062037
PRIOR FILING DATE: 1997-10-10
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-24
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Best Local Similarity 99.3%;
Matches 1474; Conservative
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ORGANISM: Homo sapiens
S-10-211-858-11
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Sequence 11, Application US/10211858
Publication No. US20030211096A1
GENERAL INFORMATION:
APPLICANT: Achkenazi, Avi J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Scot A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanab
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RESULT 7
US-10-305-654-41
; Sequence 41, Application US/10305654
; Publication No. US20030224984A1
; GENBRAE INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hans-Peter
APPLICANT: Gerber, Mary E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, J.
; APPLICANT: Pan, J.
; APPLICANT: Stephan, J-P F.
; APPLICANT: Watanabe, C.K.
; APPLICANT: Watanabe, C.K.
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APPLICANT: Williams, P.M.
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235R1C1
CURRENT APPLICATION NUMBER: US/10/305,654
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 41
LENGTH: 2482
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                                                                                               Score 1468; DE
Pred. No. 0;
0; Mismatches
                                                                                              Query Match
Best Local Similarity 99.3%;
Matches 1474; Conservative
                                                                   ; TYPE: DNA
; ORGANISM: Homosapiens
US-10-305-654-41
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J. Sequence 9, Application US/10245103

Sequence 9, Application US/10245103

Publication No. US2003068778A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Fator of Eaton, Dan

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin

APPLICANT: Gurney, Austin

APPLICANT: Sephan, Jean-Phillippe

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: APPLICANT: ASSAME

FILE REFERENCE: P3630R1112

CURRENT APPLICATION NUMBER: US/10/245,103

CURRENT PILING DATE: 2002-09-17

PRIOR PILING DATE: 2002-07-18

PRIOR PILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/063046
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Pred. No. 0;
0; Mismatches
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PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/065027

PRIOR FILING DATE: 1997-11-10

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-05-22

PRIOR FILING DATE: 1998-06-02

PRIOR FILING DATE: 1998-06-02

PRIOR FILING DATE: 1998-06-02

PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-24

PRIOR PILING DATE: 1998-06-24

PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removnumber of SEQ ID NOS: 116

SEQ ID NO 9

LENGTH: 2482

TYPE: DNA

ORGANISM: Homo Sapien

US-10-245-103-9
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Best Local Similarity 99.3%;
Matches 1474; Conservative
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Pred. No. 0;
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       SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630R1C71
CURRENT APPLICATION NUMBER: US/10/245,107
CURRENT FILING DATE: 2002-09-16
PRIOR PPLICATION NUMBER: 10/197942
PRIOR PILING DATE: 1997-09-17
PRIOR PPLICATION NUMBER: 60/063046
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-20
PRIOR PILING DATE: 1997-11-20
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-05-22
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-25
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Best Local Similarity 99.3%;
Matches 1474; Conservative
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US-10-245-107-9
                                                                                                                                                                                                                                                                                                        ID NO 9
ENGTH: 2482
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Sequence 9, Application US/10245107

Publication No. US20030068779A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Watanbe, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
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        APPLICANT: GITMAIA, J. CHISTOPHET
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Scephan, Jean-Phillippe
APPLICANT: Scephan, Jean-Phillippe
APPLICANT: Matanba, Colin
APPLICANT: Matanba, Colin
APPLICANT: Mood, William
APPLICANT: Tahay, Zamin
APPLICANT: Pang, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMERANE POLYPEPTIDES AND NUCI
TITLE OF INVENTION: ACIDS ENCODING THB SAME
FILE REPRENCE: P3630R1C30
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 60/063046
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-24
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Pred. No. 0;
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Best Local Similarity 99.3%;
Matches 1474; Conservative
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ORGANISM: Homo Sapien
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LENGTH: 2482
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US-10-245-143-9
; Sequence 9, Application US/10245143
; Publication No. US20030068780A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
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            US-10-24-771-9

US-10-24-771-9

Sequence 9, Application US/10245771

Publication No. US20030068781A1

GENERAL INCORANTION:
APPLICANT BAKET Kevin
APPLICANT Grimaldi, C. Christopher
APPLICANT Sephan, Jean-Phillippe
APPLICANT Sephan, Jean-Phillippe
APPLICANT Stephan, Jean-Phillippe
APPLICANT Stephan, Jean-Phillippe
APPLICANT Road, William
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ITILE OF INVERTION: ACIDS ENCODING THE SAWE
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TILE OF INVERTION: ACIDS ENCODING THE SAWE
FILE REFERENCE: 2042-09-16
FRICE RETLING DATE: 1297-09-16
FRICE RILING DATE: 1297-09-16
FRICE RILING DATE: 1297-10-24
FRICE RILING DATE: 1297-10-10
FRICE RILING DATE: 1298-06-18
FRICE RILING DATE: 1298-06-18
FRICE RILING DATE: 1298-06-24
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FRICE RETLING DATE: 1208-06-25
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Best Local Similarity 99.3%;
Matches 1474; Conservative
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; ORGANISM: Homo Sapien
US-10-245-771-9
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APPLICANT: Baxer, Kevin
APPLICANT: Elacon, Dan
APPLICANT: Elacon, Dan
APPLICANT: Filvacrif, Ellen
APPLICANT: Filvacrif, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimal, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Matanbe, Colin
APPLICANT: Matanbe, Colin
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APPLICANT: Mood, William
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APPLICANT: MOOG, William
APPLICANTON WOMER: 1097-01-01
PRIOR PLING DATE: 1997-01-07
PRIOR PLING DATE: 1997-01-07
PRIOR PLING DATE: 1998-01-07
PRIOR APPLICATION WOMER: 60/05696
PRIOR PLING DATE: 1998-06-02
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Publication No. US20030068783A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/099803

PRIOR PLINC DATE: 1998-09-10

PRIOR PLINC DATE: 1998-09-10

PRIOR PLINCATION NUMBER: 60/10534

PRIOR PLINCATION NUMBER: 60/11554

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PRIOR PLINCATION NUMBER: 60/13729

PRIOR PLINCATION NUMBER: 60/14732

PRIOR PRIOR DATE: 1999-06-20

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PRIOR PRIOR DATE: 1999-06-30

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PRIOR PILING DATE: 2000-04-25
PRIOR APPLICATION WUMBER: 60/20636
PRIOR APPLICATION WUMBER: 60/20636
PRIOR PILING DATE: 2000-06-05
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 2000-09-02
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-05
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APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Wood, William
APPLI
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Publication No. US20030073189A1
GENERAL INFORMATION:
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OR FILING DATE: 2001-09-04

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OR FILING DATE: 2001-11-30

OR APPLICATION NUMBER: 10/052586

OR FILING DATE: 2002-01-15

OR APPLICATION NUMBER: 10/081056

OR FILING DATE: 2002-02-20

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PRIOR FILING DATE: 1999-08-31

PRIOR APPLICATION WOMBER: 60/170262

PRIOR FILING DATE: 1999-10-29

PRIOR PLILING DATE: 1999-10-29

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PRIOR PLILING DATE: 2000-02-09

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R FILING DATE: 2001-03-09
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R FILING DATE: 2001-06-01
R APPLICATION NUMBER: 09/918585
R FILING DATE: 2001-07-30
R APPLICATION NUMBER: 09/924419
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R APPLICATION NUMBER: 09/921836
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R RILING DATE: 2002-01-15
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This DNA encodes a human secreted protein. The specification provides secreted protein sequences (AAM63681 to AAW63699) encoded by the nucleic acid sequences shown in AAV43601 to AAV43619. The invention provides a

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ALIGNMENTS

Secreted protein; human; cell proliferation; cytokine activity; tissue growth; cellular differentiation; regeneration; activin; inhibin; chemotactic; haemostatic; thrombolytic; tumour inhibition; anti-inflammatory activity; biomarker; ss. cytokine, cell proliferation tumour inhibition or anti-ഗ Kothakota "human secreted protein" Williams LT, 4 encoding DNA. having inhibin, Location/Qualifiers 171. .791 /*tag= a /product= "human seco 찞 Garcia P, 1505 97WO-US022787 96US-0032757P Secreted human polypeptides differentiation, activin or entry) differentiation, activin inflammatory activities. standard; DNA; Human secreted protein (first WPI; 1998-348453/30 P-PSDB; AAW63684. SORP Hu Q, (CHIR) CHIRON 18-JUN-1998. sapiens W09825959-A2 11-DEC-1997; 11-DEC-1996; ٿر ر 24-SEP-1998 AAV43604; AAV43604 Escobedo Ношо Key RESULT 1 AAV43604

sec

Sequence 1505 BP; 332 A; 450 C; 406 G; 317 T; 0 U; 0 Other;

540 600 9 660 720 600 360 420 480 480 540 240 420 180 240 300 300 360 0 120 120 60 9 rgagatgg |||||||| |rgagatgg STTACTGCT CACCCTG CTCCAAGA rcccaged |||||||| rcccaged TTACGGCA GGAAAGGC recedence |||||||||| |recededen GAATTCGGCACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACA Gaps CTITGAGAGGCAGCTCTGGGGCTCAGGCGACTTTCCCCCCAGGGCCCCTCCATG ACAAAGGGCACTGCGTGGACCTGCCAGACTCAGGACTCTGCAAGGAGGAGCAT(GGTACTACAACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTG. AGGATGTTTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCACAGGCTCTGT CTGTCGCAGTGTTCCTGGTCATCTGCATTGTGGTGGTGGTAGCCATCTTGGG ö DB 2; Length 1505 Indels .. Score 1505; Pred. No. 0; 0; Mismatches .. Query Match Best Local Similarity 100.0%; Matches 1505; Conservative (541 483 661 361 481 542 601 661 423 421 601 61 121 241 241 301 301 361 **.**--61 121 181 181 ठे D D 움 ò ó

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1260 1320 1200 1320 1020 1080 1140 1140 PRO256; UNQ223; human; immune disease; autoimmune disease; antirheumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic; antiasthmatic; antiallergic; immunostimulant; protease inhibitor; ss. 960 900 900 780 840 840 Trecengratergetical and a second transfer that the angering of the second transfer of the s GTGAAGAGGAGGAAGAGCCTGTTTGGCCTCTCTATCCTCTTCCTCTTCCCCCAAG GAGAAAGCTCAAAGGTTTTGGAAGGAGCAGAAACCCTTGGGCCAGAAGTACCAGACTAGA GCCCCTCTGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCCTGCTTGCCAAGG CAGAGGCCTGGGCTGGGAAAACTTTGGAACCAGACTTTTGCCTGTTTCCCAGGCCCACT CCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCACCACGC BP 82 24 cDNA encoding PR0256 entry) CDNA 1505 (first 150 standard; 30-APR-2001 LT 2 0055 AAF30055 1441 1321 1381 1441 1501 1501 1381 AAF30055 1261 1321 1201 1261 1021 1081 1081 1201 1021 1141 1141 841 901 961 961 781 841 901 721 781 Human RESULT
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Location/Qualifiers 188. .1777 /*tag= b 293. 1774 /*tag= -*tag= /*t. 188 WO200105972-A1 sig_peptide mat_peptide 25-JAN-2001

2000WO-US006884 5-MAR-2000;

99US-0144758P 20-JUL-1999;

(GETH) GENENTECH INC

Godowski PJ Pitti RM, A, SA, Goddard Marsters , Fong S, Mark MR, J, Baker KP, Hillan KJ, M Ŗ, Ashkenazi AJ Ā Watanabe Gurney

WPI; 2001-103149/11 P-PSDB; AAB20113.

useful as mult: New PRO polypeptides, nucleic acids and (ant) agonists, diagnosing and treating immune-related disorders, such sclerosis, rheumatoid arthritis and diabetes.

21; Fig 11; 127pp; English. Claim

The present sequence is that of cDNA clone DNA35880-1160 (ATCC 209379)
encoding novel human immunomodulator protein PRO256 (UNQ223) (see
AAB20113). The clone was isolated from a human placenta off with library. The
condition for the clone was isolated from a human placenta off with the clone was isolated from a human placenta off with the clone was isolated from a human placentary. The
polynoucleotides (see AAF3050-62) encoding novel human PRO proteins (see
polynoucleotides (see AAF3050-62) encoding novel human PRO proteins (see
polynoucleotides (see AAF3050-62) encoding novel human PRO proteins of inflammatory calls into a tissue of a mammal, stimulating or enhancing an
immune response in a mammal, or increasing infiltration of inflammatory calls into a tissue of a mammal, stimulating or enhancing of inflammatory calls into a tissue of a mammal, stimulating no fructions of the PRO polypeptide or its antagonist have the opposite comprising the PRO polypeptide, an agonist a real disorder, involves administering the PRO polypeptide, an agonist a rell disorder, involves administering an immune related disorder, systemic lupus erythematosus, rheumatory systemic selected from a natisagonist antibody. The disorder is systemic arthritis, spondyloarthropathy, systemic sclerosis, juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis, uttoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal diseases (such as multiple sclerosis), autoimmune chromic active hepatitis, primary biliary cirrhosis, granulomatous skin disease, (auto)immune-mediated skin diseases (such as multiple sclerosis), alternsess, (auto)immune-mediated skin diseases (such as such as arakt-versushost colitis and crohn's disease), gluten-sensitive enteropathy, Mipple's asthma, altergic rhinitis, atopic dermatitis, food hypersensitivity and associated diseases (such as graft rejection and graft-versushost colities and colones asthma, altergic chaines as graft rejection and graft-versushos 1ymphocytes disorders Also claimed cells, associated diseases (such as graft rejection and graft-versus-disease) (all claimed). Claimed methods of diagnosing these disease) (all claimed). Claimed methods of the PRO gene. All are a method of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host chantibodies and a method of stimulating the proliferation of T-

BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other; Sequence 2482

Query Match

Length 2482; DB 4; Score 1468; 97.5%;

1294 1534 488 548 608 668 728 848 908 68 69 TACCTTCGGGAAGAAGACTCCATTCTAGCCTGTCGGGGTGTGCAAGGTGGGCCTTTGAGA
1055 TACCTTCGGGAAGAAGACATTCTAGCCTGTCGGGGTGTGCAAGGTGGGCCTTTGAGA 429 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGAAC
1415 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGTTGTTATGGCAACAAGAAC AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCGCGGCATCTCCCAAGAAGGATGTG TTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCACAGGCTCTGTGGAGATGGCTGTCGCA TTTTGGCCTGTGAAATCCCAGCACAGGCTCTGTGAGATGGCTGTCACA Grottcctggtcatctgcatrgtggtggtggtagccatcttgggttactgcttcttcaag TGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCCTGCTTGCCAAGGCAGAGGCCTICCTGCTTGCCAAGGCAGAGGCCTICCTGCTTGCCAAGGCAGAGGCCCTGGCTGGCTGCTTGCCAAGGCAGAGGCAGAGGCC TCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACCTG ACTGTCTCCACTACCGAGGACACGGGGCCTGGTCTATAACCACGCGGGCCCCTC GAGACCAGGGCTCCAGCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGTCCTGAGAAGC CCTGCATAGGAGTTTGGAGTTTTGTTTTCCTCTGTTCAAAGCTGCCTGTCCT 1475 489 1535 1715 369 609 689 849 1029 얺 d 셤 셤 셤 g 8 ò ઠે 셤 ጵ ਨੇ ç 셤 셤 ద q Š ò Ş ò ठ 셤 셤 셤 Š ò ਨੇ 셤 ઠે 占

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PRO256"
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The present invention relates to PRO256 or its agonist/antagonist may be used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, especially a human with cardiac hypertrophy, trauma, a type of tumour or age-related macular degeneration. PRO256 may be administered tumour or age-related macular degeneration, or angiogenic agent, a chemotherapeutic agent, a growth inhibitory agent, or a cytotoxic agent. PRO256 may also be used to treat the disorders above, preferably through administration via ex vivo gene therapy. PRO256 or its agonist may be aministration via ex vivo gene therapy. PRO256 or its agonist may be activity of a hepatocyte growth, angiogenesis or protease activity of a hepatocyte growth factor. Stimulation or inhibition of the protease activity of a hepatocyte growth factor is protease activity of a hepatocyte growth factor is protease activity of a hepatocyte growth factor is or angiogenic disorder selected from peripheral vascular disease, hepatic or renal injury or a restinosis disorder. The present sequence is human the procyte growth factor inhibitor, PRO256 cDNA
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                                                            An isolated polypeptide designated PRO256 useful for cardiovascular, endothelial, or angiogenic disorder.
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                                                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and anglogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human PRO polypeptides of the invention
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89 GTGTGCTCTGGCACCTGTCAGCCCACCCAGTTCCGCTGCAGCAATGGCTGCTGCATCGAC 2 [[TTTCCTGGAGTGTGACGACCCCCAACTGCCCCGACGCCTCC AAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTC	11	rttgaggaagcagcagtgcctcgagtcttgtgggggggggg	1535 TTTGGCCTGAGGCGGAAATCCCCATTCCCAGCACAGGCTCTGTGGAGATGGCTGTCACA 1594 609 GTGTTCCTGGTCATTGTGGTGGTGGTAGCCATCTTTGGGTTACTGCTTCTAAG 668 1595 GTGTTCCTGGTCATTGTGTGGTGGTAGCCATCTTTGGGTTACTGCTTCTTCAAG 1654	669 AACCAGAGAAAGGACTTCCACGGACACCACCACCACCACCACCCCTGCCAGCTCC 728	729 ACTGTCTCCACTACCGAGGACACCTGGTCTATAACCACACCACGGGGCCCCTC 788	789 TGAGCCTGGGTCTCACCGGCTCTCACCTGGCTTCCTGCTTGCCAAGGCAGAGGCC 848	aaactttggaac 	909 GAGACCAGGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC 968	969 TCAAAGGTTTGGAAGAGCAGAAAACCCTTGGGCCAGAGTACCAGACTAGATGGACCTG 1028 	1029 CCTGCATAGGAGTTTGGAGTTTTGTTTCCTCTGTTCAAAGCTGCCTGTCC 1088	1089 CTACCCCATGGTGCTAGGAAGAGGAGTGGTGTCAGACCCTGGAGGCCCCAACCCT 1148	1149 GTCCTCCCGAGCTCCTCTTCCATGCTGTGCGCCCCAGGGCTGGGAAGGAA	1209 GTAGTTTGTGCTGTAAAGAGTTGCTTTTTTTTTTTAATGCTGTGGCATGGGTGAAGAG 1268	269 GAGGGGAAGAGCCTGTTTGGCCCTCTCTATCCTCTTCCTCT

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                                                                                                                                                                                                                                                                                                                                                                          ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB855003. The PRO proteins and polynucleotides have cardiant, cytostatic antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritic angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention
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  2001US-00866034.
2001WO-US017092.
2001US-00870574.
2001WO-US017443.
2001WO-US017800.
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larity 99.3%;
Conservative
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Godowski PJ, Gurney P
Stephan JF, Watanabe
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P-PSDB; ABBB4837.
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Matches 1474; Conser
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25-MAY-2001;
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infarction),
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2000US-023147P.
2000US-0235147P.
2001US-0261878P.
2001US-0261910P.
2001US-0261939P.
2001US-0264395P.
2001US-0264395P.
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2001US-0264395P.
2001US-0282129P.
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2001US-0282129P.
2001US-0280589P.
2001WO-US017092.
2001WO-US017800.
2001WO-US017869.
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                     entry)
                                  CDNA encoding human
                    (first
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22-SEP-2000;

10-NOV-2000;

12-JAN-2001;

16-JAN-2001;

16-JAN-2001;

16-JAN-2001;

25-JAN-2001;

09-FEB-2001;

09-FEB-2001;

09-FEB-2001;

09-MAR-2001;

04-APR-2001;

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04-APR-2001;

05-MAY-2001;

09-MAY-2001;

09-MAY-2001;

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09-MAY-2001;

09-MAY-2001;

09-JUN-2001;
                                                                     Homo sapiens
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                     15-JUL-2002
       ABK69965;
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INC GENENTECH (GETH)

N Grimaldi JC; Wood WI, Zhar 드 주, 유 , Goddard Watanabe C рì Filvaroff E Stephan J, OL, Eaton D γÀ Ϋ́ Gurney A Baker Fong

WPI; 2002-362426/39 P-PSDB; ABG34034.

New PRO polypeptides and polynucleotides encoding the polypeptuseful in gene therapy, chromosome identification, tissue type genetic analysis of individuals with genetic disorders.

2; Fig 9; 218pp; English Claim

This invention relates to the cDNA and protein sequences of novel
secreted and transmembrane polypeptides PRO polypeptides. The invention
also comprises a method for producing the proteins of the invention by
recombinant means and antibodies specific for the protein of the
invention. The antibody may be used for detecting the PRO proteins of the
invention and may be used to modify their activity. polynucleotides may
be used as hybridisation probes for a cDNA library to isolate the fulllength PRO cDNA or to isolate other cDNAs, to construct hybridisation
probes for mapping the gene which encodes that PRO and for genetic
analysis of individuals with genetic disorders, in assays to identify
other proteins or molecules involved in binding reaction, to generate
transgenic animals or knock-out animals which in turn are useful in the
development and screening of therapeutically useful reagents, for
chromosome identification, and tissue typing. The PRO polypeptides are
useful in gene therapy, and as molecular weight markers for protein
clectrophoresis purposes. The sequences may also be used to detect
overexpression on PRO polypeptides in cancerous tumours and for screening

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for differentially expressed present sequence represents invention
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One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction); endothelial or angiogenic disorders in a mammal.
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Pred. No. 0;
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,, Hillan KJ, M.
.K, Williams PM,
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2000US-00709238.

2000WO-US030873.

2000WO-US032678.

2000WO-US032678.

2000WO-US034956.

2001US-00767609.

2001US-00767609.

2001US-00767609.

2001US-00767609.

2001US-00808220.

2001US-00816744.

2001US-008166028.

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Best Local Similarity 99.3%;
Matches 1474; Conservative
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FERRARA N.
GERBER H.
GERRITSEN M E.
GODDARD A.
GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
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Godowski PJ, Gurney A
                                                                                                                                                                                                       GENENTECH INC
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PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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P-PSDB; ABB95443.
 08-NOV-2000;

08-NOV-2000;

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20-DEC-2000;

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22-JAN-2001;

28-FEB-2001;

28-FEB-2001;

28-FEB-2001;

09-MAR-2001;

09-MAR-2001;

10-MAY-2001;

25-MAY-2001;

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                                          CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTTGTTTCCTCTGTTCAAAGCTG
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2000US-0220624P.
2000US-0220664P.
2000WO-US020710.
2000WS-0222695P.
2000WO-US023522.
2000WO-US023328.
2000WS-0230978P.
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02-AUG-2000;
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18-SEP-2000;
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          of human
The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritiangina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention
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Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour; tumour necrosis factor-alpha; TNP-alpha; blood; chondrocyte cell; tumour; adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer; microvascular endothelial cell; endothelial cell tube formation; sports-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for stimulating proliferation of human microvascular endothelial cells, and PRO6018 polypeptide useful for stimulating proliferation of chondrocyte cells.
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Zhang
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Wood WI,
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Stephan JP,
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2001WO-US027099.
2002US-00197942.
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Smith V,
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P-PSDB; ADA01278.
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29-AUG-2001;
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                                                             GAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCG
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factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polynucleotide of the invention.
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Pred. No. 0;
0; Mismatches
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74; Conservative
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Best Local Sim:
Matches 1474;
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ADA43706
ID ADA4
XX
AC ADA4
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DT 20-N
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DE Huma
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CM BB;
KW micz
KW micz
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KW 11ve
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COS Hom
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JC; Zhang

Grimaldi J Wood WI,

Goddard A, Watanabe CK,

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Filvaroff E. Stephan JP,

e.g. gene

English

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New isolated nucleic acid encoding a PRO polypeptide, PRO21383, useful in molecular biology, chromosome and generating antisense RNA and DNA, and in gene therapy.
     2002US-00245859
               2001WO-US027099
2002US-00197942
                                                                                                 308pp;
                               INC
                                         Eaton DL,
Smith V,
                                                             2003-605867/57
B; ADA43707.
                               GENENTECH
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              29-AUG-2001;
18-JUL-2002;
                                                                                                 r
Lig
    16-SEP-2002;
                                        Baker KP,
Gurney AL,
Fong S;
                                                             WPI, 200
P-PSDB;
                               (GETH )
                                                                                                 Claim
X#X##X#X####X####X###X###X###X#
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The invention relates to an isolated secreted/transmembrane (PRO)

polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the nucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide, an extracellular domain of PRO acking its associated signal peptide, Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO Eusion proteins, inducing endothelial cell tube formation (by administering PRO2107, PRO21801, PRO1560, PRO1860, PRO499), PRO4091, PRO4091, PRO21093 can oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6108 polypeptide is useful for stimulating the proliferation of numan microvascular endothelial cells. PRO6071, PRO4897 and PRO6006 polypeptides are useful for stimulating the proliferation of numan microvascular endothelial cells. PRO6071, PRO4897 and PRO6006 calcovascular endothelial cells. PRO6071, PRO4897 and PRO6006 calcovascular endothelial cells. PRO6071, PRO489, PRO5093 and PRO389, PRO6309, P ion of an s useful as a generation of les. PRO and ines. The oligonucleotide probes are useful for isolating genomic and cDNN nucleotide sequences, for measuring or detecting the expression associated gene, and as antisense probes. PRO nucleic acid is use hybridisation probe, in chromosome and gene mapping, in the gene antisense RNA and DNA, and for the preparation PRO polypeptides PRO nucleic acid are useful as therapeutic agents, e.g. vaccines o PRO polypepi genomic and cl encodes a PRO protein present sequence

0 Length 2482; Indels 10; 8. OB Score 1468; Di Pred. No. O; O; Mismatches ö 97.5%; ilarity 99.3%; Conservative Similarity Matches 1474; Query Match Best Local 995)

709 G; 458 T; 0 U; 0 Other;

2482 BP; 523 A; 792 C;

Sequence

128 248 GFGTGCTCTGCCACCTGTCAGCCCACCCAGTTCCGCTGCAGCAATGGCTGCTC TACCTTCGGGAAGAGAGTGCATTCTAGCCTGTCGGGGTGTGCAAGGTGGGC TACCTTCGGGAAGAAGAGTGCATTCTAGCCTGTCGGGGTGTGCAAGGTGGGC 1055 ф Ф 1115 189 Б 셤 8 ð ò δ

488 548 848 968 AACCCCTTCAGCGAACACTGGCCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGAACAAAAACACTTTACCTATGGTGGTTGTTATGGCAACAAGAACAACAACAACACTTTACCTATGGTGGTTTATGGCAACAAGAAC TTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCACAGGCTCTGTGGAGATGGCTGTCGCAATTCGCCAGCACACGCTCTGTGGAGATGCCCATTCCCAGCACAGGCTCTGTGGAGATGGCTGTCACA CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGGCATCCCGCGCTGGTACTAC GTGTTCCTGGTCATCTGCATTGTGGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG GAGACCAGGGCTCCAGCCCCTCTTGGAGAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC TCAAAGGITTTGGAAGGAGCAGAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACCTG CCTGCATAGGAGTTTGGAGTTTGGAGTTTTGTTTCCTCTGTTCAAAGCTGCCTGTCCTGTTCAAAGCTGCCTGTCCTGTTCAAAGCTGCCTGTCCTGTTCAAAGCTGCCTGTCCTGTTCCTGTTCAAAGCTGCTGTTCCTGTTCAAAGCTGCTGTTCC 1475 1355 1415 549 1595 729 789 309 489 609 699 1775 1895 969 1029 1089 2075 1149 1209 2195 849 606 g 셤 d ઠે g 8 Š ठे ઠે ઠે E. ે P õ d 8 요 S ਠੋ 유 ਨੇ

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The invention relates to an isolated secreted/transmembrane (PRO)

polypeptide, having at least 80% sequence identity to a sequence selected
from any one of the 57 amino acid sequences given in specification, or to
a sequence encoded by a mucleic acid molecule selected from any one of
the nucleic acids deposited under any of the ATCC accession numbers given
the nucleic acids deposited under any of the ATCC accession numbers given
the nucleic acids deposited signal peptide, an extracellular domain of PRO
lacking its associated signal peptide, Also included are vectors,
with or without its associated signal peptide, the nucleic acids encoding
transformed host cells, anti-PRO antibodies, the nucleic acids encoding
transformed host cells, inducing endothelial cell tube formation (by
administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
an oligonucleotide probe derived from any one of the above nucleotide
sequences. PRO6018 polypeptide is useful for stimulating the
proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
                                              TTGAGCT
                              PAGCTCA
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Zhang
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GAGGGGAAGAGGCCTGTTTGGCCTCTCTGTCCTCTTCCTCTTCCCCCCAAGA
                         secreted/transmembrane polypeptide PR0256
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Stephan JF
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PRO21383 useful for stimulating
chondrocyte cells and detecting
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29-AUG-2001; 2001WO-US027099
18-JUL-2002; 2002US-00197942
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Smith V,
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B; ADA43475.
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Gurney AL,
Fong S;
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P-PSDB;
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and PRO21383 polypeptides are useful for stimulating the proliferation of human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006

polypeptides are useful for inhibiting the proliferation of human microvascular endothelial cells. PRO polypeptides are useful for detecting the presence of tumour in a mammal, including tumours of lung, colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560, PRO189, PRO6499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and PRO34274 polypeptides are useful for inducing endothelial cell tube commation. PRO or the antibody are useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide. The oligonucleotide probes are useful for isolating genomic and cDNA collectide sequences, for measuring or detecting the expression of a sesociated gene, and as antisense probes. PRO nucleic acid is useful as a hybridisation probe, in chromosome and gene mapping, in the generation of an antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence encodes a PRO protein.
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JC; Zhang

Grimaldi J Wood WI,

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Goddard Watanabe

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Filvaroff B Stephan JP,

Eaton DL, Smith V,

99US-0131271P. 99US-0162506P. 99WO-US028551. 2001WO-US027099.

2002US-00245851

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(GETH ) GENENTECH INC
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29-AUG-2001;
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2482 PRO polymucleotide #5 entry) (first standard; 06-NOV-2003 RESULT 11 ADA01149 ADA011

tumour Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumo cancer; lung; colon; breast; prostate; rectum; kidney; liver; microvascular endothelial cell; endothelial cell tube formation.

US2003068782-A1

10-APR-20,03

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, a method for stimulating the proliferation of dhondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. lung, colon, breast, prostate, rectal, kidney and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human accountion. This sequence represents a human PRO polynucleotide of the invention
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es; gene; human; PRO; secreted protein; transmembrane protein; endothelial cell tube formation; chondrocyte cell differentiation; microvascular endothelial cell; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; kidney tumour; liver tumour; cytostatic; vaccine.
                                                                  Human cDNA encoding secreted/transmembrane polypeptide PRO256
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JC; Zhang Grimaldi J Wood WI, Goddard A, Watanabe CK, щ Filvaroff B, Stephan JP, (GETH) GENENTECH INC Eaton DL, Smith V, Baker KP, Gurney AL,

02-AUG-2000; 2000US-022695P 20-JUN-2001; 2001WO-US019692 29-AUG-2001; 2001WO-US027099 18-JUL-2002; 2002US-00197942

2002US-00245143

6-SEP-2002;

10-APR-2003

US2003068780-A1

Homo sapiens

Gurney ? Fong S;

the condition responsive vaccines. e.g. PRO281 treating a coagents e.g. Novel isolated PRO polypeptides preparation of a medicament for polypeptide, and as therapeutic WPI; 2003-625485/59 P-PSDB; ADA01034.

English Claim 2; Fig 9; 307pp; The invention relates to an isolated secreted/transmembrane (PRO)

polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to sequence encoded by a mucleic acid molecule selected from any one of in specification, or a sequence having at least 80% identity to PRO in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, inducing endothelial cell tube formation (by administering PRO281, PRO1560, PRO189, PRO499, PRO6309, PRO6000, administering PRO281, PRO1560, PRO189, PRO4499, PRO6309, PRO6000, PRO1801383 polypeptide or its agonist) and an oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6018 polypeptide is useful for stimulating the pro118 PRO1313, PRO20080 and PRO51383 polypeptides are useful for stimulating the pro118 pro6006 bull microvascular endothelial cells. PRO polypeptides are useful for inhibiting the pro116 are useful for inhibiting the pro116 pro2003 and pro189, PRO4499, PRO6400, PRO10275, PRO20193 and PRO189, PRO4499, PRO6000, PRO1187, PRO20933 and PRO381474 polypeptides are useful for inducing endothelial cells to prostate, rectal, kidney and liver. PRO2033 and PRO39174 polypeptides are useful for inducing endothelial cell tube formation of a

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medicament for treating a condition responsive to PRO polypeptide. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences, for measuring or detecting the expression of an associated gene, and as antisense probes. PRO nucleic acid is useful as a hybridisation probe, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence encodes a PRO protein.
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nes 1474; Conservative
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2001WO-US015264 2001WO-US027099 2002US-00197942 02-JUN-2000; 29-AUG-2001; 18-JUL-2002;

GENERATECH INC (GETH)

N JC; Zha Grimaldi J Wood WI, Goddard A, Watanabe CK, Filvaroff B, Stephan JP, Eaton DE, Smith V, Ä 엁 Gurney Fong

WPI; 2003-585304/55 P-PSDB; ADA43591.

)2008(prigg PRO e.g. gene New isolated nucleic acid encoding a PRO polypeptide, PRO21383, useful in molecular biology, chromosome and generating antisense RNA and DNA, and in gene therapy.

9; 352pp; English ሙ •ሓ ወ .; N Claim

The invention relates to an isolated secreted/transmembrane (PWU)

Completion, having at least 80% sequence sidentity to a sequence selected

Thom any one of the 57 amino acid sequences given in specification, or to
a sequence encoded by a nucleic acid molecule selected from any one of
the incleic acids deposited under any of the ATCC accession numbers given
the incleic acids deposited under any of the ATCC accession numbers given
the sequence acids deposited whing at least 80% identity to PRO
lacking its associated signal peptide. Also included are vectors,
transformed host cells, anti-PRO antibodies, the mucleic acids encoding
PRO, PRO fewion proteins, inducing endothelial cell tube formation (by
administering PRO231, PRO1806, PRO189, PRO4499, PRO6108, PRO6108,
PRO10275, PRO2107, PRO2033 or PRO34374 Polypeptide or its agonist) and
an oligomucleotide probe derived from any one of the above nucleotide
proliferation or differentiation of chondrocyte cells. PRO1313, PRO2000

RRO10313, PRO5133 polypeptide is useful for stimulating the proliferation of
microvascular endothelial cells. PRO6101, PRO4487 and PRO6006

polypeptides are useful for stimulating the proliferation of human
microvascular endothelial cells. PRO6101, PRO4487 and PRO5006

polypeptides are useful for inhibiting the proliferation of human
microvascular endothelial cells. PRO polypeptides are useful for
polypeptides are useful for inhibiting the proliferation of human
microvascular endothelial cells. PRO polypeptides are useful for
polypeptides are useful for inhibiting endothelial cell tube
formation. PRO or the antibody are useful in the preparation of
medicament for treating a condition responsive to PRO polypeptide. The
oligomucleoride probes are useful for inducing endothelial cell tube
oligomucleoride probes are useful for propes. PRO nucleic acid suseful as a
mesociated gene, and as antisense probes. PRO mucleic acid are useful a
microsiated gene, and as antisense probes. PRO mucleic acid are useful as
alsociated gene, and as antisense and g associated gene, and as antisense probes. PRO nucleic acid is hybridisation probe, in chromosome and gene mapping, in the gentisense RNA and DNA, and for the preparation PRO polypeptide PRO nucleic acid are useful as therapeutic agents, e.g. vaccin present sequence encodes a PRO protein. are user encodes

458 T; 0 U; 0 Other; ပွဲ C; 709 792 Sequence 2482 BP; 523 A;

188 SCATCGAC ö CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAA CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAA GTGTGCTCTGGCACCTGTCAGCCCACCCAGTTCCGCTGCAGCAATGGCTGCTG Length 2482; Indels 10; DB 8; ed. No. 0; Mismatches Score 1468; Pred ; 0 97.5%; 99.3%; Conservative Query Match Best Local Similarity Matches 1474; Conser 995 1055 129 1115 1175 σı 189 日 硆

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1414 1594 1894 2074 1954 548 908 428 728 848 899 968 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCGCGGCATCTCCCAAGAAGGATGTG CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGACATCCCGGCGCTGGTACTAC GTGTTCCTGGTCATCTGCATTGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAGGTTACTGCTTCTTCAAGGTTACTGCTTCTTCAAGGTTACTGGTTACTGGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCTTAGGTTACTGCTTACTGAAGCCATCTTGGGTTACTGCTTCTTCAAG TGGGCTGGGAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCTCACTCTTGCCTCTTGCCTCTTGCCTCTTGCCTCTTGCCTGTGTCTTGCCTCTTGCCTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCC GAGACCAGGGCTCCAGCCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGTCCTGAGAAGC CCTGCATAGGAGTITTGGAGGAAGTITGGATTTTGTTTCCTCTGTTCAAAGCTGCCTGTCC 1415 489 1595 1655 1775 1835 1295 369 1475 549 535 699 1715 789 849 606 1895 696 1209 1355 2195 ઠે 셤 딘 ద d qq Š 엽 ద a ð ठ S ઠે 뭐 à 셤 셤 ਠੇ ठ Š ਨੇ 셤 ठ δ ò ò ठे 윱 ठ

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal {e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours}. The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in
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cells
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generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human condition of the invention.
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2482 entry) CDNA; secreted (first standard; Novel human 06-NOV-2003 ADA08340

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and transmembrane protein PRO256

CDNA

ss; gene; osteopathic; antirheumatic; antiarthritic; gene therapy; cell proliferation stimulator; chondrocyte cell differentiation stimulator; secreted and transmembrane protein; PRO; human; PRO1313; PRO20080; PRO21383; human microvascular endothelial cell proliferation; PRO60071; PRO4487; PRO6006; PRO240; PRO256; PRO698; PRO1002; PRO4316; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour; rectal tumour; articular cartilage defect; osteoarthritis; rheumatoid arthritis; tissue typing.

sapiens Ношо

The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (1). RR06018 polypeptide is useful for stimulating the
proliferation or differentiation of chondrocyte cells. PRO20180,

or PR02133 polypeptide is useful for stimulating the proliferation of
human microvascular endothelial cells. PR06071, PR04487, or PR0606

polypeptide is useful for inhibiting the proliferation of human
microvascular endothelial cells. PR0 POLYpeptides such as PR0206

polypeptide is useful for inhibiting the proliferation of human
microvascular endothelial cells. PR0 POLYpeptides such as PR0206

CC PR0608, PR01002, PR041316, etc., are useful for detecting the presence of
tumour in a marmal which involves comparing the level of expression of
the above mentioned polypeptides in a test sample of cells taken from the
mammal, and a control sample of normal cells of the presence of tumour
cc omparate to the control sample is indicative of the presence of tumour in
the mammal, the tumour being adrenal tumour, cervical tumour colon tumour,
the mammal, the tumour pelng adrenal tumour, cervical tumour in liver
the mammal, the tumour pelng adrenal tumour, cervical tumour or liver
tumour. PR06018 polypeptide is useful for screening compounds to
breast tumour. PR06018 polypeptide are useful for screening compounds to
comparate the propolypeptide are useful as molecular weight markers for
protein electrophoresis. (I) is also useful for screening compounds to
identify those that mimic the PR0 polypeptide (agonists) or prevent the
condition probes for a cDN library to isolate the full length in the generate either conva. Mucleotide sequences encoding RD
conva to isolate sfull other conva interportions may be used as
hypridisation probes for a cDN library to isolate the full length in the derectopement and screening of therapeutically
cuseful reagents. (II) encoding (I) or its modified forms can also be
considered either and transmembrane properties are also useful in gene
cused to generate either transgenic enably sequence encod chondrocyte Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for stimulating proliferation of human microvascular endothelial cells, PRO6018 polypeptide useful for stimulating proliferation of chondrocells. Ŋ JC; Zhang molecules are useful for tissue typing. This sequence encodes human secreted and transmembrane PRO polypeptide. Grimaldi G Wood WI, Ą,Ą Goddard Watanabe <u>,</u> Filvaroff E Stephan JP, Claim 2; Fig 9; 308pp; English. 2001US-0290589P. 2001WO-US027099. 2002US-00197942. 2002US-00245883 INC Eaton DL, Smith V, WPI; 2003-625488/59 P-PSDB; ADA08341. (GETH) GENENTECH 09-MAY-2001; 29-AUG-2001; 18-JUL-2002; 16-SEP-2002; 10-APR-2003 KP, Baker KE Gurney A Fong S;

0 Other; 0 U Ë 458 Ö ΰ 792 523 A; Sequence 2482 BP;

Gape ö 2482; Indels Length 10; 8, DB Score 1468; DE Pred. No. 0; 0; Mismatches ö Query Match
Best Local Similarity 99.3%;
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5.1.6 Compugen Ltd version - 2004 GenCore (c) 1993 Copyright

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. . AAAAAAGTCCTGCGGCCGC

US-09-935-390A-4 1505

GAATTCGGCACGAGGAGCAG..... score Title: Perfect so Sequence:

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SUMMARIES

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ALIGNMENTS

PAT 27-AUG-2002

BD063229

Secreted human proteins.

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BD063229.1 GI:22608832

JP 2001505783-A/4.

unidentified

unclassified.

E 1 {bases 1 to 1505}

Secreted human proteins

L Patent: JP 2001505783-A 4 08-MAY-2001;

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PF 11-DEC-1997 JP 1998526977
PR 11-DEC-1996 US 60/032757
PI JAIME ESCOBEDO, QUIANJIN HU, PABLO GARCIA, LB
, SRINIVAS KOTHAKOTA
PC C12N15/12, C12N15/62, C12N15/85, C12N5/10, C12
C07K16/18
CC Strandedness: Single;
CC Topology: Linear;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J.,
Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M.,
Tumas, D., Watanabe, C.K. and Wood, W.I.
Compositions and methods for the treatment of immune related
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batent: WO 0105972-A 11 25-JAN-2001;
Genentech, Inc. {US}
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Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
Patent: WO 0200690-A 41 03-JAN-2002;
Genentech, Inc. (US)
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/mol_type="unassigned DNA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Baker, K.P., Eaton, D.L., Filvaroff, E., Goddard, A., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., Wood, W.I., Zhang, Z. and Fong, S.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 2482)

Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,

Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,

Chen,J., Chow,B., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,

Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,

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Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,

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Goddard,A., Wood,W.I. and Godowski,P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale

Effort to Identify Novel Human Secreted and Transmembrane Proteins:

A Bioinformatics Assessment

L Genome Res. 13 (10), 2265-2270 (2003)
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Direct Submission
Submitted (01-AUG-2003) Department of Inc., 1 DNA Way, South San Francisco,
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Homo sapiens clone DNA35880 HAI-1
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GLRRRIPIPSTGSVEMAVTVFLVICIVVVVAILGYCFFKNQRRDFHGHHHHPPPTTPAS
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Yuan, J. and Moran, P. Direct Submission
Submitted (12-MAY-2003) Physiology, Genentech Inc, One DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2370)
Kirchhofer, D., Peek, M., Li, W., Stamos, J., Bigenbrot, C.,
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Unclassified.

I (bases 1 to 1870)

S Hillman, J.L., Tang, Y.Tom., Lal.,
Patterson, C.
Human protease associated proteins
Human protease associated proteins
Location/Qualifiers

1. 1870
/organism="unknown"
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Score 1458.6
-4. No. 0; Score 1458.6; Pred. No. 0; 0; Mimmatches 0, Query Match Best Local Similarity 99.4%; Matches 1464; Conservative G ۲. Ŋ 2370 AR1 818 966 1058 878 549 729 1118 789 398 458 638 429 609 249 698 938 699 6 69 129 518 189 578 309 369 758 489 source VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL FEATURES REFERENCE AUTHORS ORIGIN q 셤 8 a ò 덩 셤 셤 셤 ä ద ઠે 8 ਨੇ ਨੇ ઠ ò ò ò ò ઠે ò ठ

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PC C12N15/09, A61K38/00, A61R45/00, A61P19/02, A61P35/00, A61P37/02, PC C07K14/81, PC C07K16/38, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02 PC , C12Q1/68, C12N15/00, PC A61K37/02, C12N5/00, PC A61K37/02, C12N5/00, CC Incyte clone 1319265: FH Key Location/Qualifiers 1.1870	Query Match Best Local Similarity 99.4%; Pred. No. 0; Matches 1464; Conservative 0; Mismatches 9; Indels 0; Gaps 0; Qy CacGaGGAGCAGATCTGCAAGAGTTTATGGAGGCTGCTTGGCAACAAGAACAAC Db 398 CCCACGGAGCAGATCTGCTTTATGGAGGCTGCTTGGCAACAAGAACAAC Qy 69 TACCTTCGGAAGAAGAGAGTTTCTAGCTTCTCGGGCTGCTTGAGACAAC Db 458 TACCTTCGGGAAGAAGAGAGCATTCTAGCCTGTCGGGGGTGTGCAAGGTGGGCCTTTGAGA 128 Db 458 TACCTTCGGGAAGAAGAGAGCATTCTAGCCTGTCGGGGGTGTGCAAGGTGGGCCTTTGAGA 517	9 GGCAGCTCTGGGGCTCAGGCGACTTTCCCCCCAGGGCCCCTCCATGGAAAGGCGCCCATCCA 1	309 GAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCCCAGCGACAAGGG 36 [429 PACCCCTTCAGCGAACACTGGGCCCGTTTACCTATGGTGGTTGTTATGGGCAACAAGAAC 48 818 PACCCTTCAGCGAACACTGGGCCCGCTTTACCTATGGTGGTTGTTATGGCAACAAGAAC 87 489 PACTTTGAGGAAGAGCAGCGCCCGCTTTACCTTGTGGGTTGTTATGGCAACAAGAAC 87 489 PACTTTGAGGAAGAGCAGTGCCTCGAGTCTTGTCGGGCATCTCCAAGAAGATTGT 54 FITHILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504328.

Location/Qualifiers

1. .2297

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Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                             Strausberg, R. Strausberg, R. Direct Submission Submitted (01-MAR-2001) National Institutes of Health, Mammalian Submitted (01-MAR-2001) National Institutes Office, National Cancer Gene Collection (MGC), Cancer Genemics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Brin Helton, Mark Ketteman, Anuradha
Anup Madan, Jessica Fahey, Brin Helton, Mark Cetteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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U.S.A.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Proc. Natl. Acad. 3
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Homo sapiens

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Loases 1 to 2297)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

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Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I. (bases 1 to 2486)
Strausberg, R.L.; Fedingold, B.A.; Grouse, L.H.; Derge, J.G.;
Klausner, R.D.; Collins, F.S.; Wagner, L.; Shemmen, C.M.; Schuler, G.D.;
Altschul, S.F.; Zeeberg, B.; Buetow, K.H.; Schaefer, C.F.; Bhat, N.K.;
Hopkins, R.F.; Jordan, H.; Moore, T.; Marx, S.I.; Wang, J.; Hsieh, F.;
Diatchenko, L.; Marusina, K.; Farmer, A.A.; Rubin, G.M.; Hong, L.;
Stapleton, M.; Soares, M.B.; Bonaldo, M.F.; Casavant, T.E.;
Scheetz, T.E.; Brownstein, M.J.; Usdin, T.B.; Toshiyuki, S.,
Carninci, P.; Prange, C.; Raha, S.S.; Loquellano, N.A.; Peters, G.J.;
Abramson, R.D.; Mullahy, S.J.; Bosak, S.A.; McEwan, P.J.;
Morley, K.C.; Hale, S.; Garcia, A.M.; Gay, L.J.; Hulyk, S.W.;
Villalon, D.K.; Mazey, D.M.; Sodergren, E.J.; Lu, X.; Gibbs, R.A.;
Sanchez, A.; Whiting, M.; Madan, A.; Young, A.C.; Shevchenko, Y.;
Bouffard, G.G.; Blakesley, R.W.; Touchman, J.W.; Green, E.D.;
Dickson, M.C.; Rodrigues, A.C.; Grimwood, J.; Schmutz, J.; Myers, R.M.;
Butterfield, Y.S.; Krzywinski, M.I.; Schalska, U.; Schmutz, J.; Myers, R.M.;
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens serine protease inhibitor, Kunitz type 1, transcript variant 2, mRNA (cDNA clone MGC:15571 IMAGE:3140292), complete cds. BC018702.
BC018702.1 GI:17511685
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Series: IRAL Plate: 22 Row: h Column: 7.
Location/Qualifiers
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0892-2590
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Steven Jones, Jennifer Asano, Ian Bosdet, Stin Garland, Ran G
Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran G
  (2002)
                                                                                                     2 (bases 1 to 2486)
Strausberg, R.
Direct Submission
Submitted (07-DEC-2001) National Institutes of Health,
Gene Collection (MGC), Cancer Genomics Office, National Institute, 31 Center Drive, Room 11A03, Bethesda, MD 24
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inhibitors"
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197. .1738
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clone lib="NIH MGC 21"
lab host="DH10B-R"
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Natl. Acad. Sci. U.S.A.
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                        Length
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0; Mismatches
inhibitors"
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Oy 849 TGGGCTGGGAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCA 908 1775 TGGGCTGGGAAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCA 1834 Oy 909 GAGACCAGGGCTCCAGCCCCTCTTGGAAAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC 968 Oy 1835 GAGACCAGGGCTCCAGCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC 1894	Oy 969 TCAAAGGTTTGGAAGGAGCAGAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACCTG 1028	8 1 4 7 7 4 9 5 9	1209 GTAGTTTGTGCTGTAAGAGTTGCTTTTTTTTTTAATGCTGTGGCATGGGTGAAGAG 12	Db 2195 GAGGGAAGAGCCTGTTTGGCCTCTCTCTTCCTCTCCCCAAGATTGAGCT 2254 Qy 1329 CTCTGCCTTGATCAGCCCCACCTGGCCTAGACCAGGAGGAGGAGGAGAGCTCA 1388 Db 2255 CTCTGCCTTGATCAGCCCTGGCCTAGACCAGCAGACAGAGAGGCTCA 2314 Db 2255 CTCTGCCCTTGATCAGCCCTGGCCTAGACCAGCAGAGACCAGGAGAGGCTCA 2314	1389 GCTGCATTCCGCAGCCCCCACCCCCAAGG	Oy 1449 GGGTAATAAAGTGGTTTGTGGAAA 1473 	RESULT 15 AX067320 LOCUS AX067320 LOCUS DEFINITION Sequence 24 from Patent WO0078960. ACCESSION AX067320.1 GI:12544944 KEYWORDS KEYWORDS KOURCE KEYWORDS	Homo s Eukary Mammal 1 S Yuqiu, Compos	078960-A 24 28-DEC-2000; RATION (US) ation/Qualifiers .1037 ganism="Homo sapiens" 1_type="unassigned DNA"	.f="caxon:9606 '.4%; Score 1 '.9%; Pred. N

Search completed: April 22, 2004, 07:00:18 Job time : 6031 secs

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Search time 2501 Seconds (without alignments) 2459.660 Million cell updates/sec
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		BQ687222 888 bp	AGENCOURT 8047251 NIH MGC_110 Homo sapiens	5', mRNA sequence.	BQ687222	BQ687222.1 GI:21812538	EST.	Homo sapiens (human)	Homo sapiens	Sukaryota; Metazoa; Chordata; Cra	Mammalia; Butheria; Primates; Cat	1 /hogon 1 +0 000)
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

LLCM2363 row: i column: 17

High quality sequence stop: 675.

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapis-r@mail.nih.gov
Tissue Procurement: ATCC
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Homo sapiens

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Homo sapiens

Homo sapiens

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BX385810 Homo sapiene PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI005YB10 5-PRIME, mRNA sequence.

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EST.

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BX360990 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapienn clone CSODIO78YOl0 5-PRIME, mRNA sequence.

BX360990.

BX360990.1 GI:30380508

BX360900.1 GI:30380508

BY 101 Contact: Detact: Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope. Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7854.fc

Gibrary was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7854.fc

CGI-bin/Cluster.cgi?seq=CSODIO78BH05QP1&cluster=7854.fc

CGI-bin/Cluster.cgi?seq=CSODIO78BH05QP1&cluster=7854.fc

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LOCATION COMPATION COMPA
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Eukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1201)

2. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

L. Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

Email: seqrefegenoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7854.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi/seq=CSIMI002ZB06CP1&cluster=7854.f. Contact:

Feng Liang Email: fliang@lifetech.com URL:

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi/seq=CSIMI002ZB06CP1.

Feng Liang Email: fliang@lifetech.com URL:

http://www.genoscope.com.invitrogen.com/ Invitrogen. Corporation 1600

Faraday Avenue Genoscope sequence ID: CSIAI002EB06CP1.

Location/Qualifiers

1. 1201

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/clone="CSODIO05FBIO"

/clone="CSODIO05FBIO"

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/clone="Ib="Homo sapiens PlaCENTA COT 25-NORMALIZED"

/clone="Ib="Homo sapiens PlaCENTA COT 25-NORMALIZED"

/clone="Ib="Homo sapiens Placentard cDNA was grimed with a NotI-oligo (dr)

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/ beck="r" / best="Top10F'"
//lab host="Top10F'"
//clobe lib="S20T665307"
//clobe lib="S20T665307"
//note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with B. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10f' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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E 1 (Bases 1 to 635)

I (Bases 1 to 635)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

21C Frontier Korean BST Project 2001

L Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Center

Korea Research Institute of Bioscience & Biotechnology

Korea Research Institute of Bioscience & Biotechnology

Fax: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 7 row: H column: 10

High quality sequence stop: 635.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      BM820520

K-BST0089070 S20T665307 Homo sapiens cDNA clone S20T665307-7-H10
5', mRNA sequence.
BM820520
BM820520.1 GI:19176933
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/sex="M"
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/organism="Homo sapiens"
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/mol type="mana"
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/clone lib="MAPcL"
/note="vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleost;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 862)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can bifound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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hTERT-HME1, LNCap"
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/clone_lib="MAPCL"
/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
                                                         : EST 14-NOV-2002
IMAGE:6720133 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Wammalian Gene Collection (MGC)
National Institutes of Health, Wammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14279 row: c column: 13
High quality sequence stop: 598.
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92.07%
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AGENCOURT 10809135 N
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Homo sapiens (human)
Homo sapiens (human)
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 925)
NIH-MGC http://mgc.nci.nlh.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbz-rémail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
plate: LLMA10410 row: 1 column: 09
High quality sequence stop: 655.
Location/Qualifiers
1.925
//organism="Homos sapiens"
//ab host="mRNA"
//ab nost="mRNA"
//ab nost="mRN
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleosto
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 {bases 1 to 663}
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Conservative:
Mismatches:
Indels:
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/clone lib="NCI CGAP Skn3"
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/rechnologies. Note: this is a NCI_CGAP Library."
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Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10700 row: h column: 07

High quality sequence stop: 662.

Location/Qualifiers
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                             teleostomi;
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7854.f For
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Rammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1201)

I (bases 1 to 1201)

Enti W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7854.f F

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODIO30AC12QP1&cluster=7854.f. Contact Cgi-bin/cluster-cgi?seq=CSODIO30AC12QP1&cluster-7854.f. Contact Cgi-bin/cluster-cgi?seq=CSODIO30AC12QP1.

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CSODIO30AC12QP1.
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                                  EST
                                COT 25-NORMALIZED Homo
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                              BX336602
BX336602 Homo sapiens PLACENTA COCLONE CS0DI030YE23 5-PRIME, mRNA BX336602
BX336602.1 GI:30339518
EST.
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Homo sapiens
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
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RcoR1; cDNA made by oligo-dT priming. Directionally
cloned into BcoR1/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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601589675F1 NIH MGC_7 Homo sapiens cDNA clone IMAGE:3943699 5',
                                                                                                                         484
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                                                                             365 GATGTGTTTGGCCTGAGGCGGGAATCCCCATTCCCAACACACAGGCTCTGTGGAGATGGCT
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Group Phase I & II Team.

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Nature 420, 563-573 (2002)

B (bases 1 to 2155)

B (bases 1 to 2155)

Radchi,J., Alzawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Salto,H., Sakai,C., Sakai,K., Saho,H., Sasaki,D., Shibata,X., Shibata,Y., Shibata,Y., Tagawa,A., Takahashi,F., Tanaka,T., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Suzuki,H., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Direct Submission and Hayashizaki,Y.

Direct Submission and Chemical Research (RIKEN), Laboratory for Genome Physical and Chemical Research (RIKEN) (RIKEN Yokohama Institute, 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama Lastitute, 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama Lastitute, Institute, Institu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library"
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system--384-format genome Res. 10 (11), 1757-1771 (2000)
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/db_xref="taxon:10090"
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/clone_lib="RIKEN_full-length_enr
                                                                                                                                                                                                                                                                      FANTOM Consortium.
Functional annotation of a full-length
Nature 409, 685-690 (2001)
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Righ-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new gene Genome Res. 10 (10), 1617-1630 (2000)

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Mus musculus 6 days neonate head cDNA, RIKEN full-length enrilibrary, clone:5430425N02 product:serine protease inhibitor, type 1, full insert sequence.
                                                                                                                                                                                                                                                                                                                                    CysTyrGlyAsnLysAsnAsnPheGluGluGluGluGlnGlnCysLeuGluSerCy.
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Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Marmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eli, M.B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cD013

Li, M.B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cD03

Lontact: Genoscope

Genoscope - Centre National de Sequencage

Ep 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Invitrogen. This sequence belongs to sequence cluster 7854.f For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi.bin/cluster.cgi?seq=CSOBAF036ZG12 AF03456 L&cluster=7854.f.

contact: Peng Liang Email: fliang@lifetech.Com URL:

cortaction/Qualifiers

l. 948

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// mol_type="mRNA"

// db_xref="mRNA"
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// cell type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
// cell type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
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Homo sapiens cDNA clone C
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                          /note="unnamed protein product; putative
serine protease inhibitor, Kunitz type 1
(MGD | MGI:1338033) "
/codon start=1
/protein_id="BAB30697.1"
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MGIDLKVQLQKPLVLNBADNTDWHLLQGDSDVRVERKRPBEVELWGLKBGTYLFQLTR
TDSDQPEETANLTITVLTAKQTEDYCLASYKVGRCRGSFPRWYYDPKEQICKSFTFGG
CLGNKNNYLREBECMLACKDVQGISPKRHHPPVCSGSCHATQFRCSNGCCIDGFLRCDD
TPDCPDGSDEATCEKYTSGFDELQNIHFLSDKGYCAELPDTGFCKENIPRWYNPFSE
RCARFTYGGCYGNKNNFPEEQQCLBSCRGISKKDVFGLRRBGSIPTVGSAEVALAVFL
VICIIVVLTILGYCFFKNQRKEFHSPLHHPPPTPASSTVSTTEDTEHLVYNHTTQPL"
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/note="putative"
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Coordinated Laboratory for Computational Genomics
University of lowa
375 Newton Road, 4156 MEBRF, lowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Tim Ratlift
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
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CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLONE Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
The following repetitive elements were found in this cDNA
sequence: 426-483, > (TGG)n#Simple_repeat (matched compliment)
Seg primer: PVX-5.
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homi
1 (bases 1 to 647)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches
discovery
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/note="Organ: Prostate; Vector: pT7T3 Pac; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pT7T3 Pac vector. The library tag sequence located between the Not I site and the polyA tail is CCCAC. Tissue was provided by Tim Ratlift."
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BX334952 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI009YC11 3-PRIME, mRNA sequence.
BX334952
BX334952.1 GI:30310380
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Homo sapiens
Rukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J.
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AUTHORS
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Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 BVRY cedex - France
BP 191 91006 BVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI009AB06NPI&cluster=7854.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DI009AB06NPI.
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR I sites of the pCMVSPORT 6 vector. Library was normalized.
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Search completed: April 22, 2004, 10:13:59 Job time : 2508 secs

score:

Title: Perfect

Sequence

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Run on:

table:

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Minimum Maximum

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US-09-742-201-1
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APPLICANT: Escobedo, Jaime
Quianjin, Hu
Garcia, Pablo
Williams, Lewis T.
Kothakota, Srinivas
TITLE OF INVENTION: Secreted Human Pr
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BALENT PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Verence TOPPLICATION DATA:
APPLICATION NUMBER: US/09/765,449
FILING DATE: 22-Jan-2001
PRIOR APPLICATION NUMBER: 08/685,558
FILING DATE: <Unknown>
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 1542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
                                                                                                          NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MA
STREET: 2100 Pennsylvania Avenue,
CITY: Washington
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US-09-765-449-8
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: MKN45
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Gaps:
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US-10-081-056-41

Sequence 41, Application US/10081056

Publication No. US20040043927A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerber, Hanspeter

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Hillan, Wenneth J.

APPLICANT: Hillan, Wenneth J.

APPLICANT: Watanabe, Colin K.

APPLICANT: 
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Sequence 1, Application US/09742201

Patent No. US20020123091A1

GENERAL INFORMATION:

APPLICANT: Gurney, Austin L.

APPLICANT: Kirchhofer, Daniel K.

APPLICANT: Wood, William I.

TITLE OF INVENTION: No. US20020123091A1el Inhi

TITLE OF INVENTION: for Use in Modulation of

FILE REFERENCE: P1861R1US

CURRENT APPLICATION NUMBER: US/09/742,201

CURRENT FILING DATE: 2000-12-19

PRIOR PILING DATE: 2000-02-11

PRIOR PILING DATE: 2000-03-15

PRIOR FILING DATE: 2000-03-15

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 1

LENGTH: 2482
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LENGTH: 2482 TYPE: DNA ORGANISM: Homosapiens

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Gaps:
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US-10-245-752-9
; Sequence 9, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Smith, Victoria
; APPLICANT: Swith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Fong, Sherman
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Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Matanbe, Colin
APPLICANT: Matanbe, Colin
APPLICANT: Matanbe, Colin
APPLICANT: Abang, Zemin
APPLICANT: Pong, Sherman
APPLICANT: NVERTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R.C78
CURRENT APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 1092-07-08
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-14
PRIOR PILING DATE: 1997-10-10-10
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-06-02
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Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 116
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PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
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Publication No. US20030064474A1
GENERAL INFORMATION:
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Filvaroff, Ellen
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Gaps:
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630RIC66
CURRENT APPLICATION NUMBER: US/10/245,752
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 1097-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1998-05-2
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-25
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US-10-211-858-11
Sequence 11, Application US/10211858
Publication No. US20030211096A1
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Swith, Victoria
APPLICANT: Swith, Victoria
APPLICANT: Swith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: P2931RIC1
CURRENT FILING DATE: 1996-04-01
PRIOR FILING DATE: 1996-04-01
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Gaps:
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PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/062037
PRIOR FILING DATE: 1997-10-10
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR PILING DATE: 1997-11-24
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; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo sapieng
US-10-211-858-11
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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; ORGANISM: Homo Sapien
US-10-245-103-9
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                                                                             APPLICANT: Baker, Kevin P.
APPLICANT: Gerber, Hand-Peter
APPLICANT: Gerber, Hand-Peter
APPLICANT: Gerritsen, Mary B.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Glane, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Harsters, Scot A.
APPLICANT: Harsters, Scot A.
APPLICANT: Harsters, Scot A.
APPLICANT: Watanabe, C.K.
APPLICANT: Wood, W.I.
APPLICANT: Wood, W.I.
APPLICANT: Williams, P.M.
APPLICANT: WILLIA
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Matches:
Conservative:
Mismatches:
Indels:
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                                                      Sequence 41, Application US/10305654 Publication No. US20030224984A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
CACACCGGGCCCTC 1774
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Best Local Similarity:
Query Match:
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LENGTH: 2482
TYPE: DNA
ORGANISM: Hom
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Sequence 9, Application US/10245107

Fublication No. US20030068779A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Eaton, Dan

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Shang, Zemin

APPLICANT: Eong, Sherman

IITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND

FILE REFERENCE: P3630RIC71

FILE REFERENCE: P3630RIC71

FILE REFERENCE: P3630RIC71

FILE REFERENCE: P3630RIC71
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Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/245,107
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
              US-09-935-390A-23 (1-206) x US-10-245-103-9
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Matches:
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
REMAINING PATE: 1998-06-25
REMAINING PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
REMAINING PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
REMAINING PRIOR APPLICATION NUMBER: 60/090689
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; ORGANISM: Homo Sapien
US-10-245-107-9
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Query Match:
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Pred. No.:
Score:
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LENGTH: 2482
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APPLICANT: Endishell
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APPLICANT: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE REPERENCE: P3630RLC90
CURRENT APPLICATION NUMBER: U5/10/245,143
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 00/059114
PRIOR APPLICATION NUMBER: 00/063046
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/09699
PRIOR APPLICATION NUMBER: 60/09699
PRIOR APPLICATION NUMBER: 60/09690
PRIOR APPLICATION NUMBER: 60/09690
PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/09801
PRIOR FILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/090689
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PRIOR PILING DATE: 1998-06-05
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CICANT: Filvaroff, Ellen
CICANT: Goddard, Audrey
CICANT: Grimaldi, J. Christopher
CICANT: Gurney, Austin
CICANT: Smith, Victoria
CICANT: Stephan, Jean-Phillippe
CICANT: Watanbe, Colin
CICANT: Watanbe, Colin
CICANT: Pong, Semin
CICANT: Fong, Sherman
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Sequence 9, Application US/10245143
Publication No. US20030068780A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed:
NUMBER OF SEQ ID NOS: 116
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US-10-245-851-9
; Sequence 9, Application US/1024;
; Publication No. US20030068782A1
; GENERAL INFORMATION:
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APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Gaton, Dan
APPLICANT: Gariandia, J. Christopher
APPLICANT: Gordand, Audrey
APPLICANT: Gordand, Audrey
APPLICANT: Gordand, Audrey
APPLICANT: Gariandia, J. Christopher
APPLICANT: Saith, Victoria
APPLICANT: Saith, Victoria
APPLICANT: Matanbe, Colin
APPLICANT: Acnob, Sharman
APPLICANT: Tanay, Zemin
APPLICANT: Tonay, Sharman
APPLICANT: Acnob, Sharman
APPLICANTON NUMBER: 60/05014
PRIOR PLILNG DATE: 1997-10-10
PRIOR PLILNG DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/08649
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APPLICANT: Goddard, Audrey
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APPLICANT: Goddard, Audrey
APPLICANT: Gornald, J. Christopher
APPLICANT: Gurnel, Austin
APPLICANT: Grimald, J. Christopher
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
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APPLICANT: Stephan, Jean-Applicant
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                                       Sequence 9, Application US/10245883;
Publication No. US20030068783A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
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; Publication No. US20030073188A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Austin
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
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R FILING DATE: 1999-08-03

RR APPLICATION NUMBER: 60/148513

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RR APPLICATION NUMBER: 60/149327

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RR FILING DATE: 1999-08-17

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RR FILING DATE: 1999-08-31

RR APPLICATION NUMBER: 60/19651

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RR FILING DATE: 1999-08-31

RR FILING DATE: 2000-02-02

RR APPLICATION NUMBER: 60/19651

RR FILING DATE: 2000-03-03

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RR FILING DATE: 2000-05-23

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RR FILING DATE: 2000-05-23

RR APPLICATION NUMBER: 60/20985

RR FILING DATE: 2000-09-01

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RR APPLICATION NUMBER: 60/20190

RR FILING DATE: 2000-09-01

RR APPLICATION NUMBER: 60/20190

RR FILING DATE: 2001-09-01

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RR APPLICATION NUMBER: 60/20190

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R APPLICATION NUMBER: 60/26
R FILING DATE: 2001-04-04
R APPLICATION NUMBER: 60/26
R PILING DATE: 2001-04-04
R APPLICATION NUMBER: 60/29
R APPLICATION NUMBER: 60/29
          PRIOR
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                 ), Sherman
ON: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
ON: ACIDS ENCODING THE SAME
                                                                                                     : US/10/237,535
  APPLICANT: Fong, Sherman
TITLE OF INVENTION: BECESTED AND TRANS
TITLE OF INVENTION: ACIDS ENCODING TH
FILLS COF TO THE TOTAL TO NUMBER: 10/197942
PRIOR PELICATION NUMBER: 60/065014
PRIOR PELICATION NUMBER: 60/065014
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PRIOR PELICATION NUMBER: 60/065014
PRIOR PELICATION NUMBER: 60/065019
PRIOR PELICATION NUMBER: 60/06507
PRIOR PELING DATE: 1997-0-1-10
PRIOR PELING DATE: 1998-06-28
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R FILING DATE: 1999-08-25

R APPLICATION NUMBER: 09/403297

R FILING DATE: 1999-10-18

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R PILING DATE: 2002-02-20

R PILING DATE: 2002-04-09

R PILING DATE: 2002-01-15

R PILING DATE: 2002-01-15
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RESULT 1
US-08-685-558A-8
is Sequence 8, Application US/0868558A
j Patent No. 6225081
general information:
APPLICANT: SHIMOMURA, Takeshi
APPLICANT: KITAMURA, Naomi
APPLICANT: KITAMURA, Naomi
APPLICANT: KITAMURA, Reiji
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037
US-09-688-489-14
US-09-020-956-37
US-09-439-313-37
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
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FILING DATE: 24-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JPA Hei 7-187135
FILING DATE: 24-JUL-1995
FILING DATE: 24-JUL-1995
FILING DATE: 24-JUL-1995
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LENGTH: 1542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                               NAME/KEY: coding sequence
LOCATION: 1 to 1542
IDENTIFICATION METHOD: by experiment
NAME/KEY: signal peptide
LOCATION: 1 to 105
IDENTIFICATION METHOD: by experiment
NAME/KEY: mature peptide
LOCATION: 106 to 1542
IDENTIFICATION METHOD: by experiment
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Percent Similarity:
Best Local Similarity;
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: HOME
STRAIN: MKN4 F
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Sequence 8, Application US/09765449
Patent No. 6465622
GENERAL INFORMATION:
APPLICANT: SHIMOMURA, Takeshi
KAWAGUCHI, Toshiya
KITAMURA, Naomi
MIYAZAWA, Keiji
AITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
AND METHOD OF PRODUCING THE PROTEIN
                                                                                                                                                                                                                           ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,449
FILING DATE: 22-Jan-2001
PRIOR APPLICATION DATA:
                                                                                                                             NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
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Mismatches:
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Matches:
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FILING DATE: <Unknown>
INPORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 1542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: cDNA to mRNA
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: MKN45
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Sequence 14, Application US/09020956

Patent No. 6261562

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMM
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 F
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
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Percent Similarity:
Best Local Similarity:
Query Match:
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ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: WINGER: US/09/071,709
FILING DATE: Filed Herewith
CLASSIFICATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0513 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION A45-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                  TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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TOPOLOGY: lin
IMMEDIATE SOURCE
LIBRARY: BLAD
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Pred. No.:
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i Sequence 14, Application US/09439313

j Patent No. 6329505

j GENERAL INFORMATION:
    APPLICANT: Xu, Jiangchun
    APPLICANT: Dillon, Davin C.
    APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Harlocker, Susan Louise
    APPLICANT: Reed, Steven G.
    APPLICANT: Relos, Michael
    APPLICANT: Retter, Mark
    APPLICANT: Solk, John
    APPLICANT: Solk, John
    APPLICANT: Obay, Craig
    APPLICANT: Obay, Craig
    APPLICANT: Obay, Craig
                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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                             Version
           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
PILING DATE: 25-PEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Waki, David J.
REGISTRATION NUMBER: 210121.427C3
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
Query Match:
DB:
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Sequence 14, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
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Mismatches:
Indels:
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.427C2
REFERENCE/DOCKET NUMBER: 210121.427C2
REGISTRATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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10 Columbia Center,
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity:
Query Match:
DB:
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STREET: 6300 C
CITY: Seattle
STATE: WA
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; OTHER INFORMATION: n
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US-09-352-616A-14/C

i Sequence 14, Application US/09352616A

j Patent No. 6395278

j GENERAL INFORMATION:

j APPLICANT: Dillon, Davin C.

j APPLICANT: Harlocker, Susan Louise

j APPLICANT: Jiang, Yuqui

j APPLICANT: Mitcham, Jennifer Lynn

j APPLICANT: Mitcham, Jennifer Lynn

j TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAFY AND DIAGNOSIS

TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.427C8

CURRENT APPLICATION NUMBER: US/09/352,616A

CURRENT PILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 472

SOFTWARE: FabtSEQ for Windows Version 3.0
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Matches:
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 816
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                                                                                                                             NAME/KEY: misc feature;
LOCATION: (1)...(816);
OTHER INFORMATION: n =
US-09-439-313-14
                                                                                            TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity
Query Match:
DB:
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ORGANISM: Homo s
FEATURE:
NAME/KEY: misc_f
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ENGIH: 816
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Pred. No.:
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US-09-232-149A-14/c

US-09-232-149A-14/c

Sequence 14, Application US/09232149A

Batent No. 6465611

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.427C6

CURRENT APPLICATION NUMBER: US/09/232,149A

CURRENT FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 338

SOFTWARE: FastSEQ for Windows Version 3.0
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Conservative:
Mismatches:
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Gaps:
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NAME/KEY: misc feature
LOCATION: (1)...(816)
OTHER INFORMATION: n =
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TYPE: DNA
ORGANISM: Homo sapien
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SEQ ID NO 14
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Oraig H.
APPLICANT: Oraig H.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 816
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                                                                                                                                                                     US-09-636-215-14/c
; Sequence 14, Application US/0963621;
; Patent No. 6620922;
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                     Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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NAME/KEY: misc feature

LOCATION: (1)...(816)

COTHER INFORMATION: n = A,T,C

US-09-636-215-14
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ORGANISM: Homo sapien
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Best Local Similarity:
Query Match:
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US-09-159-812-14/c
; Sequence 14, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USB
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
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ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(816)
OTHER INFORMATION: n = 1
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SEQ ID NO 14
LENGTH: 816
TYPE: DNA
ORGANISM: Home
FEATURE:
LOCATION: (1)
COTHER INFORMA
US-09-159-812-14
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                                                                  Sequence 14, Application US/096884
Patent No. 6664377
GENERAL INFORMATION:
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| NAME/KEY: misc_feature
| LOCATION: (1)...(816)
| OTHER INFORMATION: n = A,T,C
US-09-115-453-14
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                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapien
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Best Local Similarity:
Query Match:
DB:
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US-09-688-489-14/c
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US-09-685-166A-14/C

US-09-685-166A-14/C

Sequence 14, Application US/09685166A

Patent No. 6630305

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchum

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Robert A.

APPLICANT: Handerson, Robert A.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, Jamuel

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICAN
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NAME/KEY: misc feature
LOCATION: (1) ... (816)
OTHER INFORMATION: n = A
US-09-685-166A-14
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RESULT 12
US-09-115-453-14/c
; Sequence 14, Application US/09115453B
; Patent No. 6657056
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 3.0
; SRQ ID NO 14
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Mismatches:
Indels:
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    Version
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
REFERENCE/DOCKET NUMBER: 210121.427C2
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: CDNA
US-09-020-956-37
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Matches:
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US-09-030-607-37/c
; Sequence 37, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IM
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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CITY: Seatt]
STATE: WA
COUNTRY: USP
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    APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427D2
CURRENT APPLICATION NUMBER: US/09/688,489
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 816
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Conservative:
Mismatches:
Indels:
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Sequence 37, Application US/09020956

Patent No. 6261562

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR INUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 70:
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                        CURRENT FILING DATE: 200
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Wi
SEQ ID NO 14
LENGTH: 816
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(816)
OTHER INFORMATION: n = A
US-09-688-489-14
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Query Match:
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Conservative:
Mismatches:
Indels:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIPICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linears
TOPOLOGY: linears
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** April 22, 2004, 04:43:13 Run on:

Search time 123 Seconds (without alignments) 6790.253 Million cell updates/sec

US-09-935-390A-4 1505 1 GAATTCGGCACGACG

GAATTOGGCACGAGGAGCAG......AAAAAAAGTCCTGCGGCCGC score: Title: Perfect so Sequence:

1505

table: Scoring

IDENTITY NUC Gapop 10.0 ,

682709 seqs, 277475446 residues Gapext 1.0 Searched:

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1365418

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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 /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:* 40m4m0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

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	1	Appli	Appli	Appli	Appl	Appl	App1	App1	App1	App1	Appl	Appl	App1	App1	Appl	, Appl	Appl	Appl	App1	Appi	Appl	, Appl	Appl	Appl	, Appl	O.	Appl .	, Appl
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SUMMARIES	ΩI	-071-	5-55	5-44	-020-95	-030-	-439-313	-09-352-61	-232-14	US-09-159-812-14	-215	-685-166A	-115-45	8-489-1	-09-020-95	-030-607-3	39-313-3	-352-616A-	-09-232-149A-	-09-159-812-3	-636-21	85-16	-09-115-453-	-09-688-489-	-020-95	US-09-030-607-15	US-09-439-313-15	Ī
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Query Match
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches

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ALIGNMENTS

RESULT 1	US-U9-U/L-/U9-b	; Patent No. 6171790 C. and	GENERAL INFORMATION:		, APPLICANT: Fang, I. Lom	Corley, Neil	••	on, Chandra	INVENTION: H	, NUMBER OF SEQUENCES: 12	ซ	EE: INCITE PHARMACEUILCADS,	ü	14	Ü	-	4304	COMPUTER READABLE FORM:	<u> </u>	IBM PC	0S/MS-DOS	; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2	; CURRENT APPLICATION DATA:	APPLICATION NUMBER: US/09/071,709	; FILING DATE: Filed Herewith	; CLASSIFICATION:	\geq	_		Æ.	; TELEPHONE: (650) 855-0555	, INFORMATION FOR SEQ ID NO: 6:	HARACTERIST	H: 1870 1	Ü	Ki.	; TOPOLOGY: linear	တ္ထ	Y: BLAD	; CLONE: 1319265	US-09-071-709-6	
RESULT 3	OS-US-US-US-	; Patent	; GENER	, API	AP	API	API	; API	TI	EDN		**	**J	7.	**	•	,.	Ö 	-				 5		••	••	; AT		 ••	TE	•-	 INFO	SE :	14	••	•	•-,	ÄH ',	••	٠.,	110,000	0 0 0

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9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAAC 6	TATGGGGGTGTGCAAGGTGGGCCTTTGAGA 12:	29 GGCAGCTCTGGGGCTCAGGCGACTTTCCCCCAGGGCCCCTCCATGGAAGGCGCCATCCA 18	GIGIGCICTGGCACCIGICAGCCCACCCAGTICCGCIGCAGCAAIGGCIGCTGCIGCAICG	249 AGTTTCCTGGAGTGTGACGACACCCCCAACTGCCCCGACGCCTCCGACGAGGCTGCCTGT 308	309 GAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATTTCCCCAGCGACAAAGGG 368 	369 CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCGCTGGTACTAC 428 	429 AACCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAGAAC 488	489 AACTTTGAGGAAGAGCAGCAGCCTCGAGTCTTGTCGCGGCATCTCCAAGAAGGATGTG 548 	549 TTTGGCCTGAGGGGGAAATCCCCATTCCCAGCACAGGCTCTGTGGAGATGGCTGTCGCA 608 	609 GIGITCCIGGICAICIGCAITGIGGIGGIGGIAGCCAICIIGGGITACTGCTICTICAAG 668 	669 AACCAGAGAAAGGACTTCCACGGACACCACCACCCACCCA	729 ACTGICICCACTACCGAGGACACGGAGCACCTGGICTATAACCACGCGCGGCCCCTC 788	789 TGAGCCTGGGTCTCACCGGCTCTCACCTGGCTTCCTGCTTGCCAAGGCAGAGGCC 848	849 TGGGCTGGGAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCA 908 	909 GAGACCAGGGCTCCAGCCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC 968	969 TCAAAGGTTTGGAAGGAGCAGAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACCTG 1028 	1029 CCTGCATAGGAGTTTGGAGGAAGTTTTGTTTCCTCTGTTCAAAGCTGCCTGTCC 1088 	
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SGAGAGCTCA 1388 ||||| ||||| SGAGAGGCTCA 1777 PGGTGAAGAG 1268 |||||||||||| |GGGTGAAGAG 1657 1328 1717 1448 1837 1208 1597 AGATTGAGCT CCCGCCCACT ACTTCCCTGT |||||||||| |ACTTCCCTGT δ

Takeshi Toshiya

SHIMOMURA, KAWAGUCHI,

in.

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NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIATE: DC
COUNTRY: USA
ZIATE: DC
COUNTRY: USA
ZIATE: DC
COUNTRY: USA
ZIATE: DC
COMPUTER READABLE FORM:
MEDIUW TYPE: Ploppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ploppy Disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ploppy Disk
COMPUTER: APPLICATION NUMBER: US/09/765,449
FILING DATE: 22-Jan-2001
PRIOR APPLICATION NUMBER: 08/685,558
FILING DATE: CURROWN:
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERSTICS:
LENGTH: 1542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: TING BATE: Acuble
                                  KITAMURA, Naomi
MIYAZAWA, Keiji
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR
AND METHOD OF PRODUCING THE PA
                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
ULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: MKN45
NO. 6465622
RAL INFORMATION:
APPLICANT: SHIMO
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                                                                                   Score 667.4; DB 3
Pred. No. 3.3e-168
); Mismatches 6
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IDENTIFICATION METHOD: by e NAME/KEY: signal peptide LOCATION: 1 to 105
IDENTIFICATION METHOD: by e NAME/KEY: mature peptide LOCATION: 106 to 1542
IDENTIFICATION METHOD: by e
                                                                                    44.3%;
ilarity 93.1%;
Conservative
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                                              Gaps
                                             48;
                              Length 1542
                                              Indels
                              Query Match
Best Local Similarity 93.1%; Pred. No. 3.3e-168
Matches 729; Conservative 0; Mismatches 6
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(ix) FEATURES:
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RESULT 3 US-09-765-449-8 ; Sequence 8, Application US/09765449

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APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
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                       CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAAC
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ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
Mismatches
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US-09-030-607-14/c
; Sequence 14, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
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             ACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCACACCACCGG
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Sequence 14, Application US/09020956

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
NUMBER OF SEQUENCES: 178

CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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STATE: CONTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RE-Lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIPICATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELEBHOKE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: single
''near
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Pred. No. 1.3e-100
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Local Similarity
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  ; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KBY: misc_feature
; LOCATION: (1)...(816)
; OTHER INFORMATION: n = A
US-09-439-313-14
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TYPE: DNA
ORGANISM: Homo sapien
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Best Local Similarity
Matches 459; Conser
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US-09-439-313-14/c

US-09-439-313-14/c

Sequence 14, Application US/09439313

Patent No. 6329505

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan Louise

APPLICANT: Reed, Steven G.

APPLICANT: Reed, Steven G.

APPLICANT: Reed, Steven G.

APPLICANT: Relos, Michael

APPLICANT: Ranger, Gary

APPLICANT: Ratter, Mark

APPLICANT: Retter, Mark

APPLICANT: Retter, Day, Craig

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THEI

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C9

CURRENT APPLICATION NUMBER: US/09/439,313

CURRENT APPLICATION NUMBER: US/09/439,313

CURRENT PILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 575

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                 Score 413.4; DB 3;
Pred. No. 1.3e-100;
); Mismatches 37;
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il Similarity 92.0%;
459; Conservative
; TYPE: B16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-030-607-14
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Best Local S
Matches 459
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Gaps
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Sequence 14, Application US/09352616A;
Patent No. 6395278;
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Aiang, Yuqui
APPLICANT: Aiang, Yuqui
APPLICANT: Mitcham, Jennifer Lynn
ITTLE OF INVENTION: OPPROSTATE CANCER AND DIAGNOSIS
ITTLE OF INVENTION: OP PROSTATE CANCER AND METHODS FOR THEIR USF
ITTLE OF INVENTION UNMBER: US/09/352,616A;
CURRENT APPLICATION NUMBER: US/09/352,616A;
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-159-812-14/C
US-09-159-812-14/C
Sequence 14, Application US/09159812A
Patent No. 6613872
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR
FILE REFERENCE: 210121.428C5
CURRENT APPLICATION NUMBER: US/09/159,812A
CURRENT FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 306
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 816
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(816)
OTHER INFORMATION: n = A,T,C or G
US-09-159-812-14
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.es 37;
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Pred. No. 1.3e
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US-09-232-149A-14/c

Sequence 14, Application US/09232149A

Patent No. 6465611

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A

CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338

SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.3e-100;
0; Mismatches 37;
                                   Score 413.4; DB 4;
Pred. No. 1.3e-100;
0; Mismatches 37;
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Matches 459; Conservative
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FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(816)
OTHER INFORMATION: n = P
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   ; OTHER INFORMATION:
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SEQ ID NO 14
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Sequence 14, Application US/09636215

Sequence 14, Application US/09636215

Patent No. 6620922

GENERAL INFORMATION:

APPLICANT: Witchar, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Ralos, Michael D.

APPLICANT: Retter, Marc W.

APPLICANT: Retter, Marc W.

APPLICANT: Retter, Marc W.

APPLICANT: Retter, Day, Craig H.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Wedvick, Thomas S.

APPLICANT: Wang, Aijun

APPLICANT: Wang, Aijun

APPLICANT: Wang, Aijun

APPLICANT: Wang, Aijun

APPLICANT: Webler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE

CURRENT APPLICATION NUMBER: US/09/636,215

CURRENT FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 852

SOFTWARE: FastSEQ for Windows Version 3.0

SEG ID NOS: 850 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 413.4; DB 4;
Pred. No. 1.3e-100;
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LOCATION: (1)...(816)
OTHER INFORMATION: n =
99-636-215-14
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US-09-685-166A-14/C
US-09-685-166A-14/C
Sequence 14, Application US/09685166A
Patent No. 6530365
GENERAL INCRAMITON:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Ranger, Wudul
APPLICANT: Ranger, Gary R.
APPLICANT: Ranger, Gary R.
APPLICANT: Ranger, Gary R.
APPLICANT: Renger, Gary R.
APPLICANT: Renger, Gary R.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Day Craig H.
APPLICANT: Carter, Day Craig H.
APPLICANT: Scolk, Tohn A.
APPLICANT: Scolk, Yasir A.W.
APPLICANT: Scolky, Yasir A.W.
APPLICANT: Scolky, Yasir A.W.
APPLICANT: Scolky, Yasir A.W.
APPLICANT: Bogiky, Yasir A.W.
APPLICANT: Bogiky, Yasir A.W.
APPLICANT: Bogiky, Yasir A.W.
APPLICANT: Bogiky, Yasir A.W.
APPLICANT: Bogiky William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSI
CURRENT APPLICATION NUMBER: 210121.427021
CURRENT APPLICATION NUMBER: 2000-10-10
SEQ ID NO 14

LENGTH: 816
TYPE: NNA
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ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(816)
OTHER INFORMATION: n =
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                                                                                                                 GAGGCAGCTCTGGGGGCGCCCTTTTCCCCCCAGGGCCCCTCCATGGAAAGGCGCCATC
CCCNCGGAGCAGATNTGCAAGAGTTT-GTTTANGGGGNTGGNTTGGGCAACAAGAANAAC
                                           GAGGCAGNINIGGGGNICAGGGACTITCCCNCAGGGCCCNINNCAIGGAAAGGCGCCAIC
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APPEICANT: Dillon, Davin C.
APPEICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427D2
CURRENT APPLICATION NUMBER: US/09/688,489
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
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Pred. No. 1.3e-100;
0; Mismatches 37;
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; Sequence 14, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
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Best Local Similarity 92.0%;
Matches 459; Conservative
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ORGANISM: Homo sapien
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OTHER INFORMATION: n
-09-688-489-14
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                            Length
                                                  Indels
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Pred. No. 1.3e-100;
0; Mismatches 37;
                          Score 413.4; DB 4;
Pred. No. 1.3e-100;
; Mismatches 37;
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US-09-115-453-14/c
Sequence 14, Application US/09115453B
Patent No. 6657056
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNO
TITLE OF INVENTION: METHODS FOR THEIR US
FILE REFERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115,45
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.
LENGTH: 816
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Local Similarity 92.0%;
nes 459; Conservative
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                          Query Match
Best Local Similarity 92.0%;
Matches 459; Conservative
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; NAME/KEY: misc feature;
; LOCATION: (1)...(816)
; OTHER INFORMATION: n =
US-09-115-453-14
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ORGANISM: Homo sapien
     US-09-685-166A-14
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Matches 459
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               TIGGITTGNIGGAGGNIGCTIGGGCAACAAGAACAACTACCITTGGGAAGAAGAGGTGCAI
                                                                                                        CCACCCAGTTCCGCTGCAGCAATGGGCTGNTGNATCGACAGTTTAGTGGAGTGTGACGAC
                                                   CTTTGAGAGGCAGCTCTGGGGCTCAGGCGA
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US-09-030-607-37/C
is Gequence 37, Application US/09030607
is Bequence 37, Application US/09030607
is Patent No. 626245
is GENERAL INFORMATION:
APPLICANT: Nu. Jiangchun
APPLICANT: Nu. Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OP
NUMBER OF SEQUENCES: 224
CORRESONDENCE ADDRESS: 224
CORRESONDENCE ADDRESS: 224
CORRESONDENCE ADDRESS: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
IPPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEADABLE FORM:
ADTICATION TYPE: Ploppy disk
COMPUTER: Datentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
LEBEPOTE: LEBUTES
LEBUTH: CSC CHARACTERISTICS:
LEBUTH: CSC Dates Dates
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nucleic acid
bedness: single
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TOPOLOGY: Linear
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US-09-030-607-37
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ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNBY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTATION NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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; Sequence 37, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; VUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; TITLE OF COLUMbia Center, 701 Fifth Avenue
; CITY: Seattle
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Pred. No. 8.4e-86;
); Mismatches 39
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Best Local Similarity 90.2%;
Matches 432; Conservative
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STATE: W
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Query Ma Best Loc Matches	Query Match Best Local Similarity 90.2%; Pred. No. 8.4e-86; Matches 432; Conservative 0; Mismatches 39; Indels 8; Gaps 5;
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Dþ	476 TIGGITIGNIGGAGGNIGCTIGGGCAACAACAACTACCTTIGGGAAGAAGAAGAIT 417
È	91 TICTAGCCTGTCGGGGTGTGCAAGGTGGGCCTTTGAGAGGCAGCTCTGGGGCTCAGGCGA 150
С	416 TICTAGCCTGTCGGGGTGTGCAAGGT-GGCCTTTGAGAGGCAGTTTGGGNTNAGGN 362
È	151 CTTTCCCCCAGGGCCCCTCCATGGAAAGGCGCCATCCAGTGTGCTCTGGCACCTGTCAGC 210
qq	361 GATTTCCCCCAGGCCCTTCCATGGAAAGGC-CNATCCAGTGTGTTCTGGCACCTGTCAGC 303
λŏ	211 CCACCCAGTTCCGCTGCAGTAT-GGCTGCTGCATCGACAGTTTCCTGGAGTGTGACGAC 269
셤	302 CCACCCAGTTCCGCTGCAGCAATGGGCTCNTGNATCGACAGTTTAGTGGAGTGTGAGGAC 243
È	270 ACCCCCAACTGCCCCGACGCCTCCGACGAGGCTGCCTGTGAAAATACACGAGTGGCTTT 329
අදු	242 ACCCCCAACTGCCCGGANGCTTCGGAGGAGGCTGCNTGTGAAAATACACGAGTGGNTTN 183
Š	330 GACGAGCTCCAGCGCATCCATTTCCCCAGCGACAAAGGGCACTGCGTGGACCTGCCAGAC 389
ą _C	182 GACGAGCTCCAGCGCATCCATTTCCCCAGTGACAAAGGGCATTGCGTGGACCTGCCAGAC 123
Š	390 ACAGGACTCTGCAAGGAGGATCCCGCGCTGGTACTACAACCCCTTCAGCGAACACTGC 449
Q,D	BACTCTGCAAG
δλ	450 GCCCGCTTTACCTATGGTGGTTGTTACGGCAACAACAACTTTGAGGAAGAAGAAGAACAACTTTTGAGGAAGAGCAGCA 508
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Search completed: April 22, 2004, 08:12:04 Job time : 125 secs

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ore version 5.1.6 993 - 2004 Compugen	g sw model 0:22:35 ; Search time (without ali	OFRCS	ext 60.0	25971 residues		chosen parameters:		5 summaries	AA:* ata/2/iaa/5A_COMB.pep:* ata/2/iaa/5B_COMB.pep:* ata/2/iaa/6A_COMB.pep:* ata/2/iaa/6B_COMB.pep:* ata/2/iaa/FCTUS_COMB.pe	results predicted by I to the score of the of the total score di	SUMMARIES		
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	pplicat 71790 RMATION Hillm Tang, Lal, Corle Guegl Guegl Guegl Guegl SEQUENC 3174 P SEQUENC 3174 P SEQUENC GENT INC 3174 P SEQUENC 10N NUN GENT INC GENT INC GENT INC 348 and MINC 110N NUN 1319265	imilarit ; Conse
	-709-2 No. 617 No. 617 L INFOIT ICANT: I	Match scal Si
. CCEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE	ESULT 1 S-09-071-709-2 Sequence 2, Application US Patent No. 6171790 GENERAL INFORMATION: APPLICANT: Tang, Y. To APPLICANT: Tang, Y. To APPLICANT: Guegler, Ka APPLICANT: Guegler, Ka APPLICANT: Patterson, TITLE OF INVENTION: HU NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PE STREET: PALO ALTO STATE: CALIFORNIA CONFUTER: BALO ALTO STATE: CALIFORNIA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy COMPUTER: IBM PC CON OPERATING SYSTEM: PC SOFTWARE: WORD PERFE CURRENT APPLICATION DAI APPLICATION NUMBER: FILING DATE: Filed F CLASSIFICATION: ATTORNEY/AGENT INFORMAT NAME: CERRONE, MICHE REGISTRATION NUMBER: REFERENCE/DOCKET NUME TELEPHONE: (650) 855 TELEFAX: (650) 845-4 INFORMATION FOR SEQ ID NG SEQUENCE CHARACTERISTIC LENGTH: AMBEDNESS: SINGLE TOPOLOGY: linear INMEDIATE SOURCE: LIBRARY: BLADNOTO4 CLONE: 1319265	Query Match Best Local Si Matches 206;
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                                                                                                                                                                                     APPLICANT: SHIMOMURA, Takeshi
KAWAGUCHI, Toshiya
KITAMURA, Naomi
MIYAZAWA, Keiji
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                   #1.25
                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: SUGHRUE, MION, ZINN, MACPEAK & STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
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1.5e-187;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,449
FILING DATE: 22-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,558
FILING DATE: <Unknown>
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
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100.0%; Pred. No. 1.9
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STRAIN: MKN45
; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-765-449-18
                                          PTPASSTVSTTEDTEHLVYNHTTRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                           Sequence 18, Application US/09765449
Patent No. 6465622
GENERAL INFORMATION:
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                                                                                                                               MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDBAACBKYTSGFDELQRIH
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                                                                                                                                                                                                                                                            RESULT 2
US-08-685-558A-18
i Sequence 18, Application US/08685558A
j Patent No. 6225081
j GENERAL INFORMATION:
l APPLICANT: SHIMOMURA, Takeshi
l APPLICANT: KAWAGUCHI, Toshiya
l APPLICANT: KITAMURA, Naomi
l APPLICANT: MIYAZAWA, Keiji
l TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
l TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
l NUMBER OF SEQUENCES: 18
l CORRESPONDENCE ADDRESS:
l APPLICANT: AND METHOD OF PRODUCING THE PROTEIN
l NUMBER OF SEQUENCES: 18
l CORRESPONDENCE ADDRESS:
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STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,558A
FILING DATE: 24-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JPA Hei 7-187135
FILING DATE: 24-JUL-1995
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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Pred. No. 1.5
; Mismatches
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Best Local Similarity 100.0%; I
Matches 206; Conservative 0;
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linear
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US-08-685-558A-18
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APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 182
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5208144-20
; Patent No. 5208144
; APPLICANT: SMITH, JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN
; TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA
; CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                     Indele
                                                                                                                                                                      Skin Cells
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Pred. No. 2.6e-18
); Mismatches 0
US-09-312-283C-182
; Sequence 182, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Sk
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.3
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Patent No. 6150502
GENERAL INFORMATION:
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les 21; Conser
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ORGANISM: mouse
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNSURE
                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Mouse US-09-312-283C-182
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LENGTH: 72
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0.0024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kestila, Marjo
APPLICANT: Lenkkeri, Ulla
APPLICANT: Lenkkeri, Ulla
APPLICANT: Mannikko, Minna
TITLE OF INVENTION: Nephrin Gene and Pr
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert
STREET: 300 S. Wacker Drive, Suite 3;
CITY: Chicago
, NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/396,697
; FILING DATE: 22-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 313,682
; FILING DATE: 22-FEB-1989
; SEQ ID NO:20:
; EENGTH: 38
5208144-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 11;
Pred. No.
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No.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
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Patent No. 6207811
GENERAL INFORMATION:
APPLICANT: Tryggvason, Karl
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Kestila, Marjo
Lenkkeri, Ulla
Mannikko, Minna
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11; Conservative
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RESULT 10
US-08-566-800A-37

j Sequence 37, Application US/0856800A

j Patent No. 5736364

j GENERAL INFORMATION:

j APPLICANT: Lee, Geoffrey F.

APPLICANT: Lee, Geoffrey F.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-08-566-800A-38

; Sequence 38, Application US/08566800A
; Patent No. 5736364
; Patent No. 5736364
; APPLICANT: Kelley, Robert P.
; APPLICANT: Lee, Geoffrey P.
; APPLICANT: Lee, Geoffrey P.
; TITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors
; TITLE OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEB: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: 90958B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 37:
TELECOM
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100.0%; P;
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Best Local Similarity 100
Matches 7; Conservative
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US-08-566-800A-32
Sequence 32, Application US/08566800A
Patent No. 5736364
GENERAL INFORMATION:
APPLICANT: Kelley, Robert F.
APPLICANT: Lee, Geoffrey F.
TITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
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Pred. No. 21;
); Mismatches
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; Mismatches
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18 MAR 1998
18: 435
                           APPLICATION NUMBER: US/09/040,774
FILING DATE: 18 MAR 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 97,842
TELECOMMUNICATION INFORMATION:
TELEFAX: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1241 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P095
TELECOMMUNICATION INFORMATION:
TELEFAX: 415/225-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
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7; Conservative
             APPLICATION DATA
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nes 8; Conser
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US-09-040-774-2
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Best Local S
Matches 8
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Matches 7
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Length 58;

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DB 1;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
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Score 7; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION S.

REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0958B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
TOWATH: 58 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-566-800A-44
; Sequence 44, Application US/08566800A
; Patent No. 5736364
; GENERAL INFORMATION:
; APPLICANT: Kelley, Robert F.
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Lee, Geoffrey F.
; TITLE OF INVENTION: No. 5736364el Fi
; WUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  42, Application US/08566800A
                                            0;
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                                                                                                                                                                                                                            Robert F. Robert 7
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                3.4%;
100.0%;
                                                                                                                                                                                             Sequence 42, Application US/08:
Patent No. 5736364
GENERAL INFORMATION:
APPLICANT: Kelley, Robert
APPLICANT: Lazarus, Robert
APPLICANT: Lee, Geoffrey F
TITLE OF INVENTION: No. 57
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                 Similarity 100
7; Conservative
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US-08-566-800A-39
i Sequence 39, Application US/08566800A
i Patent No. 5736364
i GENERAL INFORMATION:
APPLICANT: Lezarus, Robert R.
APPLICANT: Lee, Geoffrey F.
ITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
ZIP: 94080
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
              TYPE: 3.5 inch, 1.44 Mb floppy disk
SR: IBM PC compatible
ING SYSTEM: PC-DOS/MS-DOS
RE: WinPatin (Genentech)
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Pred. No. 21;
0; Mismatches
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FILING DATE: 04-Dec-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0958B
TELECOMMUNICATION INFORMATION:
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEK: 910/371-7168
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/566,800A FILING DATE: 04-Dec-1995 CLASSIFICATION: 514
                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0958B
TELECOMMUNICATION INFORMATION:
TELEFAX: 415/225-8228
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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Best Local Similarity 100.0%;
Matches 7; Conservative 0;
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TOPOLOGY:
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460 Point San Bruno Blvd
South San Francisco
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STREET: 46
CITY: Sout
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US-08-566-800A-45
i Sequence 45, Application US/08566800A
j Patent No. 5736364
i GENERAL INFORMATION:
j APPLICANT: Kelley, Robert A.
j APPLICANT: Lee, Geoffrey F.
j TITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors
j NUMBER OF SEQUENCES: 58
j CORRESPONDENCE ADDRESS:
j ADDRESSEE: Genentech, Inc.
street: 460 Point San Bruno Blvd
CITY: South San Francisco
j STATE: California
COUNTRY: USA
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STATE: Califor...

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
FILING DATE: US/08/566
FILING DATE: US/08/566
FILING DATE: US/08/566
FILING DATE: US/08/566
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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Pred. No. 21;
0; Mismatches
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APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0958B
TELEPHONE: 415/225-9281
TELEPHONE: 415/952-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 45:
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US-08-566-800A-44
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                                                   Score 7; DB 1;
Pred. No. 21;
0; Mismatches
                                                   Query Match
Best Local Similarity 100.0%; I
Matches 7; Conservative 0;
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-566-800A-45
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Search completed: April 22, 2004, 10:26:18 Job time : 24 secs